

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2006, 23:54:37 ; Search time 11385 Seconds  
(without alignments)  
11666.122 Million cell updates/sec

Title: SE01-458A  
Perfect score: 2077  
Sequence: 1 atcccggtcgaggattctct.....acbtcccaaaactgttggt 2077

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 6366136 seqs, 31973710525 residues

Total number of hits satisfying chosen parameters: 12732272

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 150 summaries

Database : GenEmbl.\*  
1: gb\_env:\*  
2: gb\_pat:\*  
3: gb\_ph:\*  
4: gb\_pl:\*  
5: gb\_pr:\*  
6: gb\_ro:\*  
7: gb\_sts:\*  
8: gb\_sy:\*  
9: gb\_un:\*  
10: gb\_vi:\*  
11: gb\_ov:\*  
12: gb\_rtg:\*  
13: gb\_in:\*  
14: gb\_om:\*  
15: gb\_ba:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Query	Score	Match	Length	Description
1	2075.4	99.9	2077	2	CS175961 Sequence
2	2075.4	99.9	2077	5	AF420371 Homo sapi
3	2056.4	99.0	2139	2	AX818172 Sequence
4	2056.4	99.0	2139	5	AF061034 Homo sapi
5	1989.4	95.8	2514	5	BC032762 Homo sapi
6	1976.8	95.2	3454	2	CS071068 Sequence
7	1927.4	92.8	2008	5	AF420373 Homo sapi
8	1845.6	88.9	2464	5	AK055403 Homo sapi
9	1779.4	85.7	1856	5	AF420372 Homo sapi
10	1779.4	85.7	2318	5	BC013876 Homo sapi
11	1747.8	84.2	2076	5	AY228374 Macaca mu
12	1730.8	83.3	1734	2	CQ771153 Sequence
13	1672.6	80.5	2681	5	AB056409 Macaca fa
14	1658.2	79.8	2671	5	AB063036 Macaca fa
15	1629.4	78.4	1925	5	AY228373 Macaca mu
16	1303	62.7	1930	14	BC102937 Bos tauru
17	1291	62.2	1799	14	AF513722 Sus scrof
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19	1101.8	53.0	2023	6	AY071834 Mus muscu
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21	1058.8	51.0	3577	6	AB069907 Rattus no
22	997.6	48.0	1897	6	BC086976 Rattus no
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26	645.2	31.1	3853	6	AB050777 Rattus no
27	644.4	31.0	2476	11	AF389351 Gallus ga
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29	629.8	30.3	1496	6	AB222073 Rattus no
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31	526.6	25.4	3454	2	CS071068 Sequence
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36	424.6	20.4	444	2	AR413165 Sequence
37	312	15.0	493	2	CQ923338 Sequence
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58	182.8	8.8	208202	12	AC013446 Homo sapi
59	180.8	8.7	397	5	AY749111S01 Macaca mu
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[illegible]



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DEFINITION	Sequence 43 from Patent WO03068268.		
ACCESSION	AX818172		
VERSION	AX818172.1	Gi:39723242	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		
AUTHORS	Ek, S., Borrebaeck, C.A. and Ehinger, M.		
TITLE	Treatment&comma; diagnosis and imaging of disease		
JOURNAL	Patent: WO 03068268-A 43 21-AUG-2003;		
	BIOINVENT INTERNATIONAL AB (SE)		
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Qy	241	AAATGTCCTCAAAATGTAAGTGGAGAAAGTGGGCACTTTTGGAGTCTTTTCCACAG	299
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Qy	360	GTGAAAGCAGAGAAATGAGACCCCTGAGTGCCTGAGTCCGCACATAGAAGATCAA	419
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AF061034 2139 bp mRNA linear PRI 09-MAY-1998  
LOCUS Homo sapiens FIP2 alternatively translated mRNA, complete cds.  
DEFINITION AF061034  
ACCESSION AF061034  
VERSION AF061034.1 GI:3127082  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 2139)  
Li, Y., Kang, J. and Horwitz, M.S.  
AUTHORS Interaction of an adenovirus E3 14.7-kilodalton protein with a  
TITLE novel tumor necrosis factor alpha-inducible cellular protein  
containing leucine zipper domains  
JOURNAL Mol. Cell. Biol. 18 (3), 1601-1610 (1998)  
PUBLISHED 9488477  
REFERENCE 2 (bases 1 to 2139)  
Li, Y., Kang, J. and Horwitz, M.S.  
AUTHORS Direct Submission  
TITLE Submitted (21-APR-1998) Microbiology and Immunology, Albert  
JOURNAL Einstein College of Medicine, 1300 Morris Park Avenue, Bronx, NY  
10461, USA

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ORIGIN

Query Match 99.0%; Score 2056.4; DB 5; Length 2139;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2071; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
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RESULT 5  
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 LOCUS  
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 ACCESSION BC032762  
 VERSION BC032762.1 GI:21619682  
 KEYWORDS MGC.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 2514)  
 STRAUSBERG, R. L., FEINGOLD, E. A., GROUSE, L. H., DERGE, J. G., KLAUSNER, R. D., COLLINS, F. S., WAGNER, L. H., SHENMEN, C. M., SCHULER, G. D., ALTSCHUL, S. F., ZEEBERG, B., BUETOW, K. H., SCHAEFER, C. F., BHAT, N. K., HOPKINS, R. F., JORDAN, H., MOORE, T., MAX, S. I., WANG, J., HSIEH, F., DATCHENKO, L., MARUSINA, K., FARMER, A. A., RUBIN, G. M., HONG, L., SCHEETZ, T. E., BROWNSTEIN, M. J., USIDIN, T. B., CASAVANT, T. L., CARLINCI, P., PRANGE, C., RAHA, S. S., LOQUELLANO, N. A., PETERS, G. J., AMERSON, R. D., MULLABY, S. J., BOSAK, S. A., MCEWAN, P. J., MCKERNAN, K. J., MALEK, J. A., GUNARATNE, P. H., RICHARDS, S., WORLEY, K. C., HALE, S., GARCIA, A. M., GAY, L. J., HULYK, S. W., VILLALON, D. K., MUZY, D. M., SODERGREN, E. J., LU, X., GIBBS, R. A., FAHEY, J., HELTON, E., KETTEMAN, M., MADAN, A., RODRIGUES, S., SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A. C., SHEVCHENKO, Y., BOUFFARD, G. G., BLAKESLEY, R. W., TOUCHMAN, J. W., GREEN, E. D., DICKSON, M. C., RODRIGUEZ, A. C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R. M., BUTTERFIELD, Y. S., KRZYWINSKI, M. I., JONES, S. J. and MARRA, M. A.  
 Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL  
 PUBLISHED 12477932  
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 STRAUSBERG, R.  
 DIRECT SUBMISSION  
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 JOURNAL

REMARK  
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 NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: ATCC  
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 DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;  
 Web site: <http://www.nisc.nih.gov/>  
 Contact: nisc\_mgc@nhgri.nih.gov  
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Clone distribution: MGC clone distribution information can be found  
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REFERENCE	1		
AUTHORS	Sornasse,T., Seilhamer,J.J. and Watson,G.A.		
TITLE	Tissue specific genes of diagnostic import		

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LOCUS  
DEFINITION  
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ACCESSION  
AK055403  
VERSION  
AK055403.1 GI:16550123  
KEYWORDS  
oligo capping; fis (full insert sequence).  
SOURCE  
Homo sapiens  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;





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LOCUS AF420372 1856 bp mRNA linear PRI 29-JUL-2003  
DEFINITION Homo sapiens optineurin isoform 2 (OPTN) mRNA, complete cds.  
ACCESSION AF420372  
VERSION AF420372.1 GI:18644683  
KEYWORDS

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
REFERENCE 1 (bases 1 to 1856)  
AUTHORS Rezaie,T., Child,A., Hitchings,R., Brice,G., Miller,L.,  
Coca-Prados,M., Heon,E., Krupin,T., Ritch,R., Kreutzer,D.,  
Crick,R.P. and Sarfarazi,M.  
TITLE Adult-onset primary open-angle glaucoma caused by mutations in  
optineurin  
JOURNAL Science 295 (5557), 1077-1079 (2002)  
PUBMED 11834836  
REFERENCE 2 (bases 1 to 1856)  
AUTHORS Sarfarazi,M. and Rezaie,T.  
TITLE Direct Submission  
JOURNAL Submitted (18-SEP-2001) Molecular Ophthalmic Genetics Laboratory,  
Surgical Research Center, Department of Surgery, University of  
Connecticut Health Center, 263 Farmington Ave, Farmington, CT  
06030-1110, USA  
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REMARK  
COMMENT

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 On Aug 19, 2003 this sequence version replaced gi:15530202.  
 Contact: MGC help desk  
 Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
 Tissue Procurement: ATCC/DCTP/DP  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Institute for Systems Biology  
<http://www.systemsbio.org>  
 contact: [amadansystemsbiology.org](mailto:amadansystemsbiology.org)  
 Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha  
 Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 14 Row: f Column: 7  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: matched mRNA gi: 20149571.

## FEATURES

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## CDS

Query Match 85.7%; Score 1779.4; DB 5; Length 2318;  
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QY 297 CAGGAATCTTGGCAATGTCCCATCAACCTTCAAGCTGCCTCACTGAAAGGAGGACGCC 356  
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DEFINITION	Macaca mulatta optineurin variant 2 (OPTN) mRNA, complete cds; alternatively spliced.		
ACCESSION	AY228373		
VERSION	AY228373.1	GI:29374063	
KEYWORDS	Macaca mulatta (rhesus monkey)		
SOURCE	Macaca mulatta		
ORGANISM	Macaca mulatta		
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REFERENCE	1 (bases 1 to 1925)		
AUTHORS	Rezaie,T., Waitzman,D.M., Seeman,J.L., Kaufman,P.L. and Sarfarazi,M.		
TITLE	Molecular cloning and expression profiling of optineurin in the rhesus monkey		
JOURNAL	Invest. Ophthalmol. Vis. Sci. 46 (7), 2404-2410 (2005)		
PUBMED	15980228		
REFERENCE	2 (bases 1 to 1925)		
AUTHORS	Rezaie,T. and Sarfarazi,M.		
TITLE	Cloning and Characterization of Optineurin in Rhesus Monkey.		
JOURNAL	Orthologue of a Glaucoma-Causing Gene in Human		
REFERENCE	3 (bases 1 to 1925)		
AUTHORS	Rezaie,T. and Sarfarazi,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-FEB-2003) Molecular Ophthalmic Genetics Laboratory, University of Connecticut Health Center, 263 Farmington Ave, Farmington, CT 06030-1110, USA		
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REMARK  
COMMENT

NIH-MGC Project  
Contact: Robert Kirkpatrick  
Canada's Michael Smith Genome Sciences Centre  
BC Cancer Agency  
Suite 100, 570 West 7th Avenue, British Columbia,  
Canada, V5Z 4S6  
Tel: 1-604-707-5900 x5406  
Tel: 1-604-876-3561  
Fax: 1-604-876-3561  
Email: robertk@bcgsc.ca  
Tissue Procurement: M. Taniguchi, Y. Meng, S. Lobo, L. Guan and S. Moore

cDNA Library Preparation: M. Masaaki, Y. Meng, S. Lobo, L. Guan  
 and Dr. S. Moore  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Bovine Genome Sequencing Program, Genome  
 Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcgsc.bc.ca  
 Moore S, Alexander L, Brownstein M, Guan L, Lobo S, Meng Y,  
 Tanaguchi M, Wang Z, Prange C, Schreiber K, Shermen C, Wagner L,  
 Ali J, Balu M, Barber S, Babakaiff R, Beland J, Chand S, Chun E,  
 Del Rio L, Gibson S, Kirkpatrick R, Liu J, Matsuo C, Mayo M,  
 Palmquist D, Santos RR, Stott J, Tsai M, Wong D, Wythoven B, Hanson  
 R, Siddiqui A, Holt R, Jones SJ, Marra MA

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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## ORIGIN

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1 (bases 1 to 1799)			
Obazawa,M., Mashima,Y., Sanuki,N., Noda,S., Kudoh,J., Shimizu,N., Oguchi,Y., Tanaka,Y. and Iwata,T.			
Analysis of porcine optineurin and myocilin expression in trabecular meshwork cells and astrocytes from optic nerve head			
Invest. Ophthalmol. Vis. Sci. 45 (8), 2652-2659 (2004)			
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2 (bases 1 to 1799)			
Sanuki,N., Obazawa,M., Mashima,Y., Tanaka,Y. and Iwata,T.			
Direct Submission			
Submitted (20-MAY-2002) National Institute of Sensory Organs, National Tokyo Medical Center, 2-5-1 Higashigaoka, Meguro, Tokyo 152-8902, Japan			
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ACCESSION BC061185  
VERSION BC061185.1 GI:38511794  
KEYWORDS MGC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridea; Muridae; Murinae; Mus.  
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Srausberg R.L., Feirgold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, M., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Scapleto, N., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Loquellano, N.A., Peters, G.J., Carninci, P., Prange, C., Raha, S.S., Loguellano, N.A., Peters, G.J., Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smaluk, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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2 (bases 1 to 2443)  
Strausberg, R.  
Direct Submission  
Submitted (03-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgaphs@mail.nih.gov](mailto:cgaphs@mail.nih.gov)  
Tissue procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Michael Brownstein / Ted Usdin  
Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-ahgc.stanford.edu>  
Contact: (Dickson, Mark) [mcdpaxil.stanford.edu](mailto:mcdpaxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 53 Row: p Column: 23  
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity to protein.  
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VERSION		AY071834.1	GI:21700320
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AUTHORS		Rezaie,T. and Sarfarazi,M.	
TITLE		Cloning and Characterization of Mouse Optineurin	
JOURNAL		Unpublished	
REFERENCE			
AUTHORS		2 (bases 1 to 2023)	
TITLE		Rezaie,T. and Sarfarazi,M.	
JOURNAL		Submitted (26-DEC-2001) Molecular Ophthalmic Genetics Laboratory,	
		Surgical Research Center, Department of Surgery, University of	
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Myokai, F.				
AUTHORS				
FIP-2 variant				
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JOURNAL				
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2 (bases 1 to 1716)				
Myokai, F. and Oyama, M.				
AUTHORS				
Direct Submission				
TITLE				
Submitted (20-JUL-2005) Fumio Myokai, Okayama University Graduate				
School of Medicine, Dentistry, and Pharmaceutical Sciences,				
Periodontal Science, Shikata-cho 2-5-1, Okayama, Okayama 700-8525,				
Japan (E-mail: myokai@md.okayama-u.ac.jp,				

Tel: 81-86-235-6677 (ex. 5678), Fax: 81-86-235-6679)				
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REFERENCE  
1 Oyama, M.  
Identification of genes expressed in rat injured dental pulp  
Unpublished  
2 (bases 1 to 3577)  
Oyama, M. and Miyokai, F.  
Direct Submission  
Submitted (11-AUG-2001) Masataka Oyama, Nagasaki University  
Graduate School of Biomedical Sciences, Division of Oral Health  
Services Research; 1-7-1 Sakamoto, Nagasaki, Nagasaki 852-8588,  
Japan (E-mail: masataka@net.nagasaki-u.ac.jp, Tel: 81-95-849-7663,  
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ORIGIN



PUBMED 12477932  
 REFERENCE 2 (bases 1 to 1897)  
 AUTHORS NIH MGC Project  
 TITLE Direct Submission  
 JOURNAL Submitted (02-DRC-2004) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Bethesda, MD 20892-2590, USA  
 REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 COMMENT Contact: MGC help desk  
 Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
 Tissue Procurement: Howard Jacobs  
 cDNA Library Preparation: Express Genomics  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www-shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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DEFINITION Sequence 15500 from Patent WO02068579.
ACCESSION CQ729566
VERSION CQ729566.1 GI:42300960
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
```

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REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 15500 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 91.7%; Pred. No. 2.5e-186;
Matches 824; Conservative 0; Mismatches 12; Indels 63; Gaps 1;
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QY 300 GAATCTCTGCAATGTCCCATCAACCTCTCAGCTGCTCACTGAAAAGGAGGACAGGCCCA 359
Db 1 GAATCTCTGCAATGTCCCATCAACCTCTCAGCTGCTCACTGAAAAGGAGGACAGGCCCA 60
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QY 420 CGGAGAGCTGTCTGACGAGATGAAAGAGCTCTCTGACCAAGAAACACACAGCTGAAAGAAAG 479
Db 121 CGGAGAGCTGTCTGACGAGATGAAAGAGCTCTCTGACCGAGAAACACACAGCTGAAAGAAAG 180
QY 480 CCATGAAGCTAAATATCAAGCCATGAAAGGGAGATTTTGAAGAGCTTTTCGGCTGACAG 539
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LOCUS BD216639 710 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel human genes and gene expression products ii.
ACCESSION BD216639
VERSION BD216639.1 GI:33026409
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KEYWORDS JP 200251900-A/4781.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 710)
REFERENCE
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D., Klinger,J.S.,
Reinhard,C., Giese,K., Randazzo,F., Kennedy,G.C., Pot,D.,
Kassam,A., Lamson,G., Drmanac,R., Crkvenjakov,R., Dickson,M.,
```



Dmanac,S., Labat,I., Leshkowitz,D., Kita,D., Garcia,V., Jones,L.W. and Crain,B.S.  
Novel human genes and gene expression products ii  
Patent: JP 2002519000-A 4781 02-JUL-2002;  
CHIRON CORP.HYSEO INC  
OS Homo sapiens (human)  
PN JP 2002519000-A/4781  
PD 02-JUL-2002  
PF 28-JAN-1999 JP 2000556580  
PR 28-JAN-1998 US 60/072910,24-FEB-1998 US 60/075954 PR  
31-MAR-1998 US 60/080114,03-APR-1998 US 60/080515 PR  
03-APR-1998 US 60/080666,21-OCT-1998 US 60/105234 PR  
28-OCT-1998 US 60/105877  
PI LOUIS T WILLIAMS,JAIME ESCOBEDO,MICHAEL A INNIS,PABLO PI  
DOMINGUEZ GARCIA,  
PI JULIE SUDDUTH KLINGER,CHRISTOPH REINHARD,KLAUSE GIESE,FILIPPO  
PI RANDAZZO,  
PI GIULIA C KENNEDY,DAVID POT,ALTAF KASSAM,GEORGE LAMSON,RADOJE  
PI DRMANAC,  
PI RADOMIR CRKVENJAKOV,MARK DICKSON,SNEZANA DRMANAC,IVAN LABAT,  
PI DENA LESHKOWITZ,DAVID KITA,VERONICA GARCIA,LEE WILLIAM JONES,  
PI BIRJIT STACHE CRAIN  
PC C12N15/09,C12N15/09,C07K14/47,C07K14/82,C07K16/18,C12N1/15, PC  
C12N1/19,  
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Best Local Similarity 98.7%; Pred. No. 2.3e-165;  
Matches 681; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
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QY 1129 GATTGAAACCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGA 1188  
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QY 1189 GACTGTTGGAAGCGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAGAGCT 1248  
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DB 682 GCAGGAAGAGG-CCTCGAAACCAATGACCAT 710  
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AR770229  
LOCUS AR770229  
DEFINITION Sequence 4781 from patent US 6964868.  
ACCESSION AR770229  
VERSION AR770229.1 GI:83345508  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 710)  
AUTHORS Williams,L.T., Escobedo,J., Innis,M.A., Garcia,P.D.,  
Sudduth-Klinger,J., Reinhard,C., Giese,K., Randazzo,F.,  
Kennedy,G.C., Pot,D., Kaessam,A., Lamson,G., Drmanac,R.,  
Crkvenjakov,R., Dickson,M., Drmanac,S., Labat,I., Leshkowitz,D.,  
Kita,D., Garcia,V., Jones,L.W. and Stache-Crain,B.  
TITLE Human genes and gene expression products II  
JOURNAL Patent: US 6964868-A 4781 15-NOV-2005;  
Nuvelo, Inc.; Sunnyvale, CA  
FEATURES  
source Location/Qualifiers  
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Query Match 32.0%; Score 665.2; DB 2; Length 710;  
Best Local Similarity 98.7%; Pred. No. 2.3e-165;  
Matches 681; Conservative 0; Mismatches 8; Indels 1; Gaps 1;  
QY 1009 GAGCCAGCTCCTGCTGCTTAAGGGAAGGGAATCAGAAGTGGAGAGCTTCAAGTTGC 1068  
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## RESULT 26

AB050777 3853 bp mRNA linear ROD 02-NOV-2002  
LOCUS Rattus norvegicus mRNA for injury-inducible-protein I-55, complete cds.  
DEFINITION

## ACCESSION

AB050777 GI:24475404

## KEYWORDS

Rattus norvegicus (Norway rat)

## SOURCE

Rattus norvegicus

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muroidae; Muridae; Murinae; Rattus.

## REFERENCE

1. Myokai, F. and Oyama, M.

Injury Inducible Gene I-55

Published Only in Database (2002)

2. (bases 1 to 3853)

Myokai, F. and Oyama, M.

Direct Submission

Submitted (03-NOV-2000) Pumio Myokai, Nagasaki University Graduate

School of Biomedical Sciences, Division of Oral Health Services

Research; 1-7-1 Sakamoto, Nagasaki, Nagasaki 852-8588, Japan

(E-mail: masataka@net.nagasaki-u.ac.jp, Tel: 81-95-849-7663,

Fax: 81-95-849-7665)

## FEATURES

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## ORIGIN

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Matches 809; Conservative 0; Mismatches 173; Indels 20; Gaps 4;

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RESULT 27

AF389351

LOCUS

VRT 16-AUG-2002

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AF389351  
AF389351.1 GI:21666286

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Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 2476)  
Stroisnigg,H., Repitz,M., Miloloza,A., Linhartova,I., Beug,H.,  
Wiche,G. and Propst,F.  
FIP-2, an IkappaB-Kinase-gamma-Related Protein, Is Associated with  
the Golgi Apparatus and Translocates to the Marginal Band during  
Chicken Erythroblast Differentiation  
Exp. Cell Res. 278 (2), 133-145 (2002)  
12169269  
2 (bases 1 to 2476)  
Stroisnigg,H., Linhartova,I., Miloloza,A., Repitz,M., Beug,H.,  
Wiche,G. and Propst,F.  
Direct Submission  
Submitted (07-JUN-2001) Institute of Biochemistry and Molecular  
Cell Biology, University of Vienna, Dr. Bohrgasse 9, Vienna A-1030,  
Austria

**FEATURES**

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**ORIGIN**

Query Match	31.0%;	Score 644.4;	DB 11;	Length 2476;
Best Local Similarity	63.2%;	Pred. No. 5.8e-160;	Mismatches 581;	Indels 63; Gaps 5;
Matches 1106;	Conservative	0;		

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QY	1677	AGGACTGGAACACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC	1736
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LOCUS	Gallus gallus AG9C5 mRNA, complete cds.		
DEFINITION	AF380358		
ACCESSION	AF380358.1	GI:14579552	
VERSION			
KEYWORDS	Gallus gallus (chicken)		
ORGANISM	Gallus gallus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;		
TITLE	Phasianinae; Gallus.		
JOURNAL	1 (bases 1 to 2555)		
PUBMED	Li, B. and Gallin, W.J.		
REFERENCE	Differential localization of chicken FIP2 homologue, Ag-9C5, in		
AUTHORS	secretory epithelial cells		
TITLE	Exp. Cell Res. 272 (2), 135-145 (2002)		
JOURNAL	11777338		
PUBMED	2 (bases 1 to 2555)		
REFERENCE	Gallin, W.J.		
AUTHORS	Direct Submission		
TITLE	Submitted (10-MAY-2001) Department of Biological Sciences,		
JOURNAL	University of Alberta, Z-631, Edmonton, Alberta T6G 2E9, Canada		
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Qy 2037 TCATTTAA 2044
Db 1701 TTAATTGA 1708

RESULT 29
AB222073
LOCUS AB222073 1496 bp mRNA linear ROD 21-JAN-2006
DEFINITION Rattus norvegicus FIP-2A variant mRNA for 14.7K-interacting
protein-2 type A variant, partial cds.
ACCESSION AB222073
VERSION AB222073.1 GI:85658722
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Murinae; Rattus.
REFERENCE 1
AUTHORS Myokai, F.
TITLE FIP-2A variant
JOURNAL Unpublished
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REFERENCE 2 (bases 1 to 1496)
AUTHORS Myokai, F. and Oyama, M.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2005) Fumio Myokai, Okayama University Graduate
School of Medicine, Dentistry, and Pharmaceutical Sciences,
Periodontal Science, Shikata-cho 2-5-1, Okayama 700-8525,
Japan (E-mail: myokai@md.okayama-u.ac.jp,
Tel: 81-86-235-6677 (ex. 6678), Fax: 81-86-235-6679)
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Location/Qualifiers
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JOURNAL					

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ACCESSION CS071068  
VERSION CS071068.1 GI:63088472  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
JOURNAL Hominidae; Homo.  
1  
Sornasse, T., Sellhammer, J. J. and Watson, G. A.  
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Patent: WO 2001032927-A 231 10-MAY-2001;  
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AX777990  
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ACCESSION AX777990  
VERSION AX777990.1 GI:32694984  
KEYWORDS Homo sapiens (human)  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
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AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
TITLE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
JOURNAL Hominidae; Homo.  
1  
Haferlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S.,  
Dugas, M., Bils, R., Brors, B. and Mergenthaler, S.  
Novel genetic markers for leukemias  
Patent: WO 03039443-A 147 15-MAY-2003;  
JOURNAL Deutsches Krebsforschungszentrum (DE);  
Ludwig-Maximilian-Universitaet Muenchen (DE);  
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QY 1909 CTTGTTTCAAAGAGGAGCTGAGAGCAGGAGCTGGCGGCAACAGCGGAATATTCGGAATTC 1968  
Db CTTGTTTCAAAGAGGAGCTGAGAGCAGGAGCTGGCGGCAACAGCGGAATATTCGGAATTC 360  
QY 1969 TTCCTGCCCCCAAGTGTGGAGAGGTTCTGCTGACATAGACAGTTACAGATTCACGTGAT 2028  
Db TTCCTGCCCCCAAGTGTGGAGAGGTTCTGCTGACATAGACAGTTACAGATTCACGTGAT 420  
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QY      2029  GGATTGCATCATTTAAGTGTTCATGATGATACCTCCCCA 2066
Db      421  GGATTGCATCATTTAAGTGTTCATGATGATACCTCCCCA 458

RESULT 33
AF049614
LOCUS      Homo sapiens huntingtin interacting protein HYPL mRNA, partial cds.
DEFINITION
ACCESSION AF049614
VERSION    AF049614.1  GI:3329430
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Faber, P.W., Barnes, G.T., Srinidhi, J., Chen, J., Gusella, J.F. and
            MacDonald, M.E.
TITLE      Huntingtin interacts with a family of WW domain proteins
JOURNAL    Hum. Mol. Genet. 7 (9), 1463-1474 (1998)
PUBMED     9702022
AUTHORS    Faber, P.W., Barnes, G.T., Srinidhi, J., Chen, J., Gusella, J.F. and
            MacDonald, M.E.
TITLE      Direct Submission
JOURNAL    Submitted (23-FEB-1998) Molecular Neurogenetics, Mass. Gen. Hosp.,
            Bldg 149, 13th Street, Charlestown, MA 02129, USA
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CDS
ORIGIN
Query Match      20.9%; Score 433.4; DB 5; Length 435;
Best Local Similarity 99.8%; Pred. No. 1.2e-103;
Matches 434; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1542  CAAGAAAAGAGTCAGAAAAGTGGACAGGGCAGTGTGAAGAACTGAGTGAATAAAGTGG 1601
Db      1     CAAGAAAAGAGTCAGAAAAGTGGACAGGGCAGTGTGAAGAACTGAGTGAATAAAGTGG 60

QY      1602  AACTGTCAGAGAAGCTCGGCTTCCAAACAGCTGCATGATGATGATGATGATGATGATGATGAT 1661
Db      61     AACTGTCAGAGAAGCTCGGCTTCCAAACAGCTGCATGATGATGATGATGATGATGATGAT 120

QY      1662  TTGCCAAGCAGGAAGAGGACCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGTTT 1721
Db      121     TTGCCAAGCAGGAAGAGGACCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGTTT 180

QY      1722  ACTGTTCTGATTTTCATGCTGAAAGAGCAGCGAGAGAGAAAATTCATGAGGAAAGGAGC 1781
Db      181     ACTGTTCTGATTTTCATGCTGAAAGAGCAGCGAGAGAGAAAATTCATGAGGAAAGGAGC 240

QY      1782  AACTGTCATGTCAGCTGGCAGTCTCTGTAAGAGATGATGATGATGATGATGATGATGATGAT 1841
Db      241     AACTGTCATGTCAGCTGGCAGTCTCTGTAAGAGATGATGATGATGATGATGATGATGATGAT 300

QY      1842  GGCAGTCCCTTGATGGAGATGCAGAGTCGTGATGGGGCGAGAAACAAGTGAATCTCTGAC 1901
Db      301     GGCAGTCCCTTGATGGAGATGCAGAGTCGTGATGGGGCGAGAAACAAGTGAATCTCTGAC 360

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QY      1902  AGGCTTACCTTGTTCAAAGAGAGAGCTGAGGACAGGAGCTGGCGCAACAGCGGAATATTC 1961
Db      361  AGGCTTACCTTGTTCAAAGAGAGAGCTGAGGACAGGAGCTGGCGCAACAGCGGAATATTC 420

QY      1962  CGATTTCATTCCTGCC 1976
Db      421  CGATTTCATTCCTGCC 435

RESULT 34
AX969999
LOCUS      Sequence 802 from Patent EP1104808.
DEFINITION
ACCESSION AX969999
VERSION    AX969999.1  GI:40976917
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Dumas Milne Edwards, J.B., Jobert, S. and Giordano, J.Y.
TITLE      ESTs and encoded human proteins
JOURNAL    Patent: EP 1104808-A 802 06-JUN-2001;
            Genset (FR)
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Best Local Similarity 98.0%; Pred. No. 2.7e-101;
Matches 438; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY      1093  TTCAGATTTTGAAAAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGAG 1152
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QY      1153  CACAGAGAAGAGATGATGAGAGAAAGGCCCGGAGACTGTTGGAAGCGAAGTGAAGC 1212
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QY      1213  ACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCAG 1272
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QY      1273  CGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAGTGTCAAGGCCCTTGAAGGAAAAA 1332
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QY      1333  TTCTGCAATTCATCAGAGTTGAATGAAGAAGCAAGAGCTTGTTTATCTAACAACAAAGTT 1392
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LOCUS	BD108718	444 bp	DNA linear PAT 18-SEP-2002
DEFINITION	EST and encoded human protein.		
ACCESSION	BD108718		
VERSION	BD108718.1 GI:23203536		
KEYWORDS	JP 2002010789-A/795		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 444)		
TITLE	Edwards,J.B.D.M., Jobert,S. and Giordano,J.E.		
JOURNAL	EST and encoded human protein		
COMMENT	Patent: JP 2002010789-A 795 15-JAN-2002; GENSET CORP OS Homo sapiens (human) PN JP 2002010789-A/795 PD 15-JAN-2002 PF 07-AUG-2000 JP 2000280989 PR 05-AUG-1999 US 60/147499 PI JEAN BAPTISTE DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE PI GIORDANO PC C12N15/09,C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19, PC C12N1/21, PC C12N5/10,C12P21/02,C12P21/08,C12Q1/68,C12N15/00,C12N5/00, PC C12N15/00 CC EST and encoded human protein FH Key Location/Qualifiers FT CDS 191..442. Location/Qualifiers source 1..444 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"		
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Best Local Similarity	98.0%; Pred. No. 2.7e-101;		
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QY	1213	ACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCAG	1272
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DEFINITION	Sequence 4538 from Patent WO2004097052.		
ACCESSION	CQ923338		
VERSION	CQ923338.1 GI:56213279		
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SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
1  
REFERENCE Burczynski, M.E., Twine, N.C., Slonim, D.K., Trepicchio, W.L.,  
AUTHORS Straßh, A., Immerman, F. and Dörner, A.J.  
TITLE Methods for prognosis and treatment of solid tumors  
JOURNAL Patent: WO 2004/097052-A 4538 11-NOV-2004;  
Wyeth (US); Burczynski, Michael E. (US)  
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QY 1656 AAACATTGCGCAAGCAGGAGGACCTGGAAACCATGACCAT-CCTGAGGCTCAGATG 1714  
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QY 1715 GAAGTTTACTGTTCTGATTTTCTGATTTTCTGATGAAAGAGCAGAGAGAGAAATTCATGAGGAA 1774  
Db 121 NNN 180  
QY 1775 AAGGAGCAACTGGCAATTCGAGCTGGCAGTCTCTGCTGAAAGAGATGATGCTTTTCGAAGAC 1834  
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Db 241 NNAGGAGGAGCTCTTGTATGAGATGCGAGTCTGATGGGCGGAGAAACAAGTGACTCT 300  
QY 1895 GACGAGGAGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGG 1954  
Db 301 GACGAGGAGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGG 360  
QY 1955 AATATTCGATTCATTTCTGCTGCCCCAAGTGTGGAGAGTTCTGCTGACATAGACAGTTA 2014  
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QY 2015 CAGATTCACGTGATGATTCATTTAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 2074  
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Db 481 GGT 483  
RESULT 38  
LOCUS BC088724  
DEFINITION Xenopus laevis hypothetical LOC496250, mRNA (cdna clone MGC:99383  
IMAGE:7205613), complete cds.  
ACCESSION BC088724  
VERSION BC088724.1 GI:56789665  
KEYWORDS MGC.

LOCUS CS135191 493 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 448 from Patent WO2005068655.  
ACCESSION CS135191  
VERSION CS135191.1 GI:72065948  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
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REFERENCE Smith, S.K.  
AUTHORS Methods of assessing a tissue inflammatory response using  
TITLE expression profiles of endothelial cells  
JOURNAL Patent: WO 2005068655-A 448 28-JUL-2005;  
Cambridge University Technical Services Limited (GB)  
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Best Local Similarity 69.2%; Pred. No. 2.5e-71;  
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QY 1955 AATATTCGATTCATTTCTGCTGCCCCAAGTGTGGAGAGTTCTGCTGACATAGACAGTTA 2014  
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QY 2075 GGT 2077  
Db 481 GGT 483  
RESULT 39  
LOCUS BC088724  
DEFINITION Xenopus laevis hypothetical LOC496250, mRNA (cdna clone MGC:99383  
IMAGE:7205613), complete cds.  
ACCESSION BC088724  
VERSION BC088724.1 GI:56789665  
KEYWORDS MGC.



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1916	CAAGAGGAGCTGAGGACAGGGA CTGGCGGCAACAGCGGAATATTCCGATTCATTCCTGC	1975
1539	GCAAGAGGGCAGCAACATGG-----AGCAGGCCAAGTATTACTGTGTATACATGT	1589
1976	CCCAAGTGTGGAGAGTTCTGCCTGACATAGACACGTTACAGATTCACTGATGGATTCG	2035
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289	Qy	CTTTTCCACAGGAACTTTCGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAGGA	348
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349	Qy	GGACAGCCCCAGTGAAGACACAGAGAAATGACCCCCCCACCTGGCCCCACCCAAACCTGGA	408
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409	Qy	CACGTTTACCCCGAGGAGCTGTGCAGCAGATGAAAGAGCTCCTGCACCAAGAACCACCA	468
203	Db	CACATTCACTCTCTGAGGAGATGCTGCAGCAAAATGAAGGAACTCTCGTTTGAGAACCACCA	262
469	Qy	GCTTGAAGAGCCATGAACTTAATTAATCAAGCCATCAAGGGAGATTTTCAGGAGCTTTC	528
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529	Qy	GGCTCTGCACAGAGAAACAGAAAGGAACGCCAGTTTTTTTGAGATACAGAGCAAGAAGC	588
323	Db	AGCTGGGCAGAGACGAGAAGGAACGACAGTTGTTTGACACACAGAAACAAAGAAGC	382
589	Qy	AAAAGAGCTCTAATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAAGCTTGAAA	648
383	Db	TAAAGAGCTCCTGATGACCTTTGAGTTATGAAATGAGAAACTGAAGGTGAGCTTTGAAA	442
649	Qy	ACTTAAAGGGAAATCAGAAAGGTCATCTGAGGACCCCACTGATGACTCCAGGGTTCCTCCAG	708
443	Db	ACTTAAGAGAGAGTCAGAAAGGCCATTTGAAGGCTCCATATGTGGCTCCAGGCCCTCCCAT	502
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RESULT	41
LOCUS	CS217029
DEFINITION	Sequence 6348 from Patent WO2005111246.
ACCESSION	CS217029
VERSION	CS217029.1 GI:83691850
KEYWORDS	.
SOURCE	Cricetulus griseus (Chinese hamster)
ORGANISM	Cricetulus griseus
PATENT	linear PAT 15-DEC-2005

## ORIGIN



AUTHORS	Almeida, J.	CDS	
	Direct Submission		
TITLE	Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,		
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk		
JOURNAL	Clone requests: clonerequest@sanger.ac.uk		
	On Nov 16, 2001 this sequence version replaced gi:16214585.		
COMMENT	The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:		
	Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at		
	http://www.sanger.ac.uk/projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at		
	http://www.sanger.ac.uk/HGP/Chr10		
	RP11-730A19 is from the library RPCI-11.3 constructed by the group of Pieter de Jong. For further details see		
	http://www.chori.org/bacpac/home.htm		
	VECTOR: pBACE3.6		
	----- Genome Center		
	Center: Wellcome Trust Sanger Institute		
	Center code: SC		
	Web site: http://www.sanger.ac.uk		
	Contact: vegas@sanger.ac.uk		
	-----		
	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.	misc_feature	
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	complement(21866..22040),		
	complement(AL353586..14:43768..45820))	misc_feature	
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bcgsc.bc.ca

Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
 Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth  
 Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,  
 Kim MacDonald, Anara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,  
 Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabhu,  
 Parvaneh Saeedi, JR Santos, Angeli Schnerch, Ursula Skalska,  
 Duane Smalilus, Jeff Stott, Miranda Tsai, George Yang, Jacque  
 Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 147 Row: O Column: 14  
 This clone was selected for full length sequencing because it  
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 VERSION AY749111.1 GI:54111692  
 KEYWORDS  
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 ORGANISM Macaca mulatta  
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 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Cercopithecoidea; Cercopithecinae; Macaca.  
 REFERENCE 1 (bases 1 to 257)  
 AUTHORS Rezaie,T., Waitzman,D.M., Seeman,J.L., Kaufman,P.L. and Sarfarazi,M.  
 TITLE Molecular cloning and expression profiling of optineurin in the rhesus monkey  
 JOURNAL Invest. Ophthalmol. Vis. Sci. 46 (7), 2404-2410 (2005)  
 PUBMED 15980228  
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 AUTHORS Rezaie,T. and Sarfarazi,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-SEP-2004) Molecular Ophthalmic Genetics Laboratory, Surgical Research Center, Department of Surgery, University of Connecticut Health Center, 263 Farmington Ave., Farmington, CT 06030-1110, USA  
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VERSION      CQ923519.1 GI:56213460
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Burczynski, M.E., Twine, N.C., Slonim, D.K., Trepicchio, W.L.,
Strahs, A., Immerman, F. and Dörner, A.J.
TITLE      Methods for prognosis and treatment of solid tumors
JOURNAL      Patent: WO 2004097052-A 4719 11-NOV-2004;
Wyeth (US); Burczynski, Michael E. (US)
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complete cds.
ACCESSION      BC055628
VERSION      BC055628.1 GI:33416920
KEYWORDS      MGC.
SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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REFERENCE      1 (bases 1 to 2075)
AUTHORS      Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Mullaby, S.J., Bosak, S.A., McEwan, P.J.,
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ACCESSION      CS135190
VERSION      CS135190.1 GI:72065947
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SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
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Hominidae; Homo.
REFERENCE      1
AUTHORS      Smith, S.K.
TITLE      Methods of assessing a tissue inflammatory response using
expression profiles of endothelial cells
JOURNAL      Patent: WO 2005068655-A 447 28-JUL-2005;
Cambridge University Technical Services Limited (GB)
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RESULT 50
LOCUS      BC055628      2075 bp      mRNA      linear      VRT 24-NOV-2004
DEFINITION      Danio rerio zgc:77868, mRNA (cdna clone MGC:66386 IMAGE:5777373),
complete cds.
ACCESSION      BC055628
VERSION      BC055628.1 GI:33416920
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SOURCE      Danio rerio (zebrafish)
ORGANISM      Danio rerio
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REFERENCE      1 (bases 1 to 2075)
AUTHORS      Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
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 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
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 Director MGC Project.  
 Direct Submission  
 TITLE  
 JOURNAL  
 PUBMED  
 AUTHORS  
 TITLE  
 JOURNAL

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgabbs@mail.nih.gov](mailto:cgabbs@mail.nih.gov)  
 Tissue Procurement: Dr. Sumio Sugano  
 CDNA Library Preparation: Dr. Sumio Sugano  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Center, Stanford University School of Medicine, Stanford, CA 94305  
 Web site: <http://www.shgc.stanford.edu>  
 Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
 Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
 R. M.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAK Plate: 122 Row: n Column: 17  
 This clone was selected for full length sequencing because it  
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 DDYDELQTFATKALADKQKIDEMKMLFKQEKDLETVSVFQAEIYSSDFVAE  
 RAAREKIHKEKRLATQLEYVYKQNSQLQEFESLGRHSMSEQRHVRPGANPQPT  
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#### ORIGIN

Query Match 9.2%; Score 191.6; DB 11; Length 2075;  
 Best Local Similarity 55.0%; Pred. No. 1.9e-39;

Matches 477; Conservative 0; Mismatches 364; Indels 27; Gaps 4;  
 QY 1190 ACTGTTGAAGCGAAGTGAAGCACTGAACCTTCAGGTGACATCTCTGTTTAAAGAGCTT 1249  
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 Db 540 AATGCTAGCACTGAGGTGAAGAACTGGAAGATCACTGTTGTTGAAGCTCTGTATGAGTTG 599  
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 QY 1250 CAAGAGGCTCATACAAAACACTCAGCAAGCTAGCTAATGAAGAAGAGACTTCAAGAAAAG 1309  
 |||||  
 Db 600 AAGCAAGCTCAGATTAAACTGACAGGCTGAGAGCATGAAGAAGAACTCGCAGGACAGA 659  
 |||||  
 QY 1310 TGTCAAGGCCCTTGAAGGAAAAAATCTGCAATTCATCAGAGTTGAATGAAGAAAGCAAGAG 1369  
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 Db 660 TGTAAAGATTGGAGCAGGATTTGGGCACTTTAAAGACTTCAGCTCGGAGACAAACAGAAG 719  
 |||||  
 QY 1370 CTGTTGTTATATACTAACAAAAAGTTAGAGCTACAGTGTGAAGAGCATGCTATCAGAAATCAA 1429  
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 Db 720 GTCCAGGCTGAGAACGACTGTCTGAAGGTTGAGATGGAAGGCTCCAAGCGCGATCAAA 779  
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 QY 1430 ATGGAACAGGCTTAAACACAGAGATGAAAAGTCCAAATTAACCTGTCTACAGATGACACAC 1489  
 |||||  
 Db 780 CTGGAACAGAGAAAGAAACCCAGATGAGAAGAGCAATCTAAACCACTGAAAGATGGGTAC 839  
 |||||  
 QY 1490 AACAAAGCTTTTCAAGAAACATAATATGCAATTGAAAAACAATTTGAGGAACTAAACAAGAAA 1549  
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 Db 840 ACCAAGCTGTTTGAAGACTACAGTGAGCTCCAGGAGGAA-----AAGAAGAAGA 888  
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 QY 1550 GAGTCAGAAAAAGTGGACAGGCACTGTGAAGAACTGTAGTGAAGAACTGGAACCTGGCACTGGCA 1609  
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 QY 1610 GAGAGGGCTCTGGCTTCCAAACAGCTGCAAAATGGAATGAATGAAGCAAAACCAATTCGCCAAG 1669  
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 Db 1008 AAGGAAAAGGATCTGGAACCATTTCTGTTTTTCAGGCACAGCAGAGATCTATTCTCTCA 1067  
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 QY 1730 GATTTTCATGCTGAAAGACGAGCAGAGAGAAAAATTTATGAGGAAAAAGGAGCAACTGGCA 1789  
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 Db 1068 GATTTCTACGCAGAAAAGAGCAGCTCGGAGAGAGATTTCAGSAGSAGAAAGAGCGTTTGGCC 1127  
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 QY 1790 TTGCAGCTGGCAGTTCTGCTGAAAGAGA-----ATGATGCTTTTCAAGACGGA 1837  
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 Db 1188 GGGAGGCATTCAATGAGCGAGATGCAAGAAGGCAATGTGCC--ACGAGGAGCCAATCCT 1244  
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 Db 1245 CAAGGGCCCCACAGCTCCAAACAACTGCTCGAGGTAGAGGTGAATGGCAGCAGCAGAAC 1304  
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 QY 1958 ATTCGAGATTCAATCTGCCCCCAAGTGTGGAGAGGTTCTGCCTGACATAGACAGCTTACAG 2017  
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 Db 1305 ATTCAGATCAGCTTGTCTTAATGTGGGAAGTCTTACCTACCTGACCTGACCTCCCTGCAG 1364  
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 QY 2018 ATTCAGTGTGATGATTCATCATCTTTAAG 2045  
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 Db 1365 ATCCACATCATGATTGCATCATCTGAG 1392  
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Search completed: May 30, 2006, 03:06:49  
 Job time : 11410 secs

Result No.	Score	Query		DB	ID	Description
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3	2075.4	99.9	2077	14	AED20542	Aed20542 Optineurin
4	2056.4	99.0	2139	10	ADL15031	Adl15031 Human FIP
5	2056.4	98.0	2139	12	ADP13343	Adp13343 Renal cell
6	2056.4	98.0	2139	13	ADR424267	Adr424267 Breast ca
7	2053.2	98.9	2108	10	ADL24738	Adl24738 Intestinal
8	2052.4	98.8	3904	13	ADP23349	Adp23349 PRO poly
9	1976.8	95.2	3454	4	AH57391	Aah57391 Human ske
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11	1927.4	92.8	2008	12	ADO43187	Ado43187 Human opt
12	1779.4	85.7	1856	9	ACF03997	Acf03997 Human opt
13	1779.4	85.7	1856	12	ADO43185	Ado43185 Human opt
14	1779.4	85.7	2327	13	ADR44212	Adr44212 Human NF
15	1779.4	85.7	2327	13	ADP23351	Adp23351 PRO poly
16	1747.8	84.2	2076	12	ADO43195	Ado43195 Macaque o
17	1730.8	83.3	1734	12	ADL14949	Adl14949 Human gla
18	1730.8	83.3	1734	14	ADW86571	Adw86571 Human opt

XX	Human, optineurin; OPN; chromosome 10; 10p14; glaucoma; ophthalmic; gene therapy; gene; ss.	Location/Qualifiers 311..2044 /tag= a /product= "optineurin isoform 1" replace(412,A) /tag= b /standard name= "single nucleotide polymorphism (SNP)" replace(433,A) /tag= c /standard name= "single nucleotide polymorphism (SNP)" replace(458,A) /tag= d /standard name= "single nucleotide polymorphism (SNP)" replace(603,A) /tag= e /standard name= "single nucleotide polymorphism (SNP)" replace(799,G) /tag= f /standard name= "single nucleotide polymorphism (SNP)" replace(911,T) /tag= g /standard name= "single nucleotide polymorphism (SNP)" replace(947,C) /tag= h /standard name= "single nucleotide polymorphism (SNP)" replace(949,C) /tag= i /standard name= "single nucleotide polymorphism (SNP)" replace(958,G) /tag= j /standard name= "single nucleotide polymorphism (SNP)" replace(1379,C) /tag= k /standard name= "single nucleotide polymorphism (SNP)" replace(1944,A) /tag= l /standard name= "single nucleotide polymorphism (SNP)"
KW	Adz00649 Mouse NEM	
XX	Adc36537 DNA encod	
XX	Adi61940 Necrosis	
OS	Adi29002 Human NEM	
XX	Adi61943 Necrosis	
PH	Adi17866 Human IKB	
FT	Adi17862 Human IKB	
FT	Adk71964 Human I K	
FT	Adq87415 Human tum	
FT	Adq86256 Human tum	
FT	Ada44712 Human inh	
FT	Ada81426 Human I-k	
FT	Aaa35027 Human ade	
FT	Aaf21149 Human low	
FT	Ada44705 Human inh	
FT	Abz96843 Human nuc	
FT	Abv75393 Human NEM	
FT	Abd20692 Human pul	
FT	Aaz07513 Human RIP	
FT	Aza07514 Human RIP	
FT	Ac23012 Human RNP	
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FT	Adf82713 Leukaemia	
FT	Abn43434 Human spl	
FT	Ach15127 Human adu	
FT	Abl05274 Drosophil	
FT	Ada71938 Rice gene	
FT	Abx41363 Bovine ES	
FT	Aaa70099 Plasmodiu	
FT	Adu01785 Novel hum	
FT	Acn54555 Cotton an	
FT	Aaa70212 Plasmodiu	
FT	Aaa10595 Gene enco	
FT	Abi00186 Human sil	
FT	Aal21312 Human bre	
FT	Acn54604 Cotton an	
FT	Aaa6749 Tumour su	
FT	Abx38235 Bovine ES	
XX	Aee04859 Cancer-as	
XX	Abt21705 Breast ca	
XX	Aac75308 Human ORF	
XX	Aaf98697 Human ova	
XX	Abx35261 Human Gef	
XX	Abx35871 Bovine ES	
XX	Acn54792 Cotton an	
XX	Abi33958 Human imm	
XX	Abx40820 Bovine ES	
XX	Abx84332 Stealth v	
XX	Abq67050 Human ang	
XX	Abi33697 Human imm	
XX	Aaa70229 Plasmodiu	
XX	Aai95036 Human neu	
XX	Aaa70096 Plasmodiu	
DR	WPI; 2003-598273/56.	
DR	P-PSDB; ABR82077.	
XX		
PT	Diagnosing the presence or absence of optineurin-associated glaucoma or optineurin-associated increased risk of glaucoma in an individual by assessing a test sample for the presence or absence of an alteration in the optineurin gene.	
PT		
PS	Claim 1; Page 68-71; 83pp; English.	
XX		
CC	The present invention describes a method (M1) for diagnosing the presence or absence of optineurin-associated glaucoma or an optineurin-associated increased risk of glaucoma in an individual comprising detecting the	
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CC presence or absence of an alteration in expression, composition or  
CC activity of an optineurin nucleic acid or polypeptide, which is  
CC indicative of the presence or absence, respectively, of the optineurin-  
CC associated glaucoma. Optineurin has ophthalmic activity and can be used  
CC in gene therapy. Optineurin therapeutic agents can be used for the  
CC manufacture of a medicament for the treatment of glaucoma or of an  
CC increased risk for glaucoma. Human optineurin is located on chromosome  
CC 10, more specifically to 10p14. The present sequence encodes human  
CC optineurin isoform 1, which is used in the exemplification of the present  
CC invention  
XX  
SQ

Sequence 2077 BP; 682 A; 431 C; 566 G; 398 T; 0 U; 0 Other;  
Query Match 99.9%; Score 2075.4; DB 9; Length 2077;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2076; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCCCGTCCGGAGTCTCTCCAGCGCGCAGGATGCCGAGAAACAGTGACCTGAGCGA 60  
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QY 61 AGCCAAGCCGGCGGCGAGGTGGCTTTGATAGTGGTGGCCACATTCCTGGCCTTGGGA 120  
DB 61 AGCCNAGCCGGCGGCGAGGTGGCTTTGATAGTGGTGGCCACATTCCTGGCCTTGGGA 120  
QY 121 TGAGCCGTA CGCCTCTGTATAACCCAACTTCTCACTTTGAAACAGCTGCTGGTTCAGC 180  
DB 121 TGAGCCGTAGCGCTCTGTATAACCCAACTTCTCACTTTGAAACAGCTGCTGGTTCAGC 180  
QY 181 ATTAATGAAGATTAGTCAGTGACGCGCTGGTGTGATAGTGGTGGCCACATAGAGAATCAA 240  
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DB 241 AAATGTCCAAAATGTAACTCGAGAGAAAGTGGCAACTTTTGGAGTGACATTTTCCACAGG 300  
QY 301 AACTTCTGCAATGTCCCATCAA CTTCTCAGCTGCCTCACTGAAAGAGGACAGCCCCAG 360  
DB 301 AACTTCTGCAATGTCCCATCAA CTTCTCAGCTGCCTCACTGAAAGAGGACAGCCCCAG 360  
QY 361 TGAAGCACAGAAATGGACCCCCCACCCTGGGCCACCCAAACCTGGACACGTTTATCCCC 420  
DB 361 TGAAGCACAGAAATGGACCCCCCACCCTGGGCCACCCAAACCTGGACACGTTTATCCCC 420  
QY 421 GGAGGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACACCCAGCTGAAGAGC 480  
DB 421 GGAGGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCGAGAACACCCAGCTGAAGAGC 480  
QY 481 CATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGGAGAGCTTTTCGGCCTGGACAGA 540  
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DB 541 GAAACAGAGGAAGAACGCCAGTTTTTGGATACAGAGCAAGAGAACGAGCGTCT 600  
QY 601 AATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAGAGCTTGGAAATCTAAAGGGAA 660  
DB 601 AATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAGAGCTTGGAAATCTAAAGGGAA 660  
QY 661 ATCAGAAAGGTCTATCTGAGAACCCCACTGATGATCTCCAGGCTTTCCAGGGCCGAAAGCGGA 720  
DB 661 ATCAGAAAGGTCTATCTGAGAACCCCACTGATGATCTCCAGGCTTTCCAGGGCCGAAAGCGGA 720  
QY 721 GCAGGAAAGGACCACTAGGACCCAGGTGGTGGAGGTACAGAGAGAGAGCAACCT 780  
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QY 901 TAGTCTTGGGCCCCACGAGAAACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGGAGCAG 960  
DB 901 TAGTCTTGGGCCCCACGAGAAACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGGAGCAG 960  
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QY 1681 CTTGGAACCATGACCATCTCAGGGCTCAGATGGAGTTTACTGTTCTGATTTTATGC 1740  
DB 1681 CTTGGAACCATGACCATCTCAGGGCTCAGATGGAGTTTACTGTTCTGATTTTATGC 1740  
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DB 1801 AGTTCTGTGAAAGAGAAATGATGCTTTTGAAGACGAGGAGCGAGCTCTTGTATGAGAT 1860  
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DB 1861 GCAGAGTCTGATGGGGGAGAACCAAGTGACTCTGACAGAGGCTTACCTGTTTCAAG 1920  
QY 1921 AGGAGCTGAGGACAGGGACTGGCGGCAACAGCGGAATATTCCGATTCTCTGCTGCCCAA 1980



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Db      1921 AGGAGCTGAGGACAGGACTGGCGGCACAGCGGAATATTCGGATTTCCTGCCCCAA 1980
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Db      2041 TTAAGTGTGTGATGATATCACTCCCAAACTGTGGT 2077
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RESULT 2
ADO43183
ID      ADO43183 standard; cDNA; 2077 BP.
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XX      29-JUL-2004 (first entry)
XX      Human optineurin isoform 1 cDNA, associated with glaucoma.
DE
XX      Human; optineurin; glaucoma; diagnosis; gene therapy; ophthalmological;
KW      gene; chromosome 10p14; ss.
XX
OS      Homo sapiens.
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XX      Key
XX      CDS
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XX      /note= "Premature stop; disease-causing alteration"
XX      replace(799,g)
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XX      /tag= o
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XX      WO2004039312-A2.
XX      13-MAY-2004.
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XX      26-JUN-2003; 2003WO-US020165.
XX
XX      25-OCT-2002; 2002US-00281457.
XX
XX      (UYCO-) UNIV CONNECTICUT.
XX      (SGEO-) ST GEORGES ENTERPRISES LTD.
XX
XX      Sarfarazi M, Rezaie T, Child AH;
XX
XX      WPI: 2004-376046/35.
XX      P-PSDB; ADO43184.
XX      GENBANK; AF420371.
XX
XX      New optineurin nucleic acids and polypeptides having sequence
XX      alterations, which indicates the presence of an optineurin-associated
XX      (risk of) glaucoma, useful for detecting or diagnosing glaucoma, e.g.
XX      primary open angle glaucoma.
XX
XX      Claim 1; SEQ ID NO 1; 110pp; English.
XX
XX      The present sequence is that of cDNA encoding isoform 1 of human
XX      optineurin (optic neuropathy inducing protein). Mutation of the
XX      optineurin gene on chromosome 10 is associated with primary open angle
XX      glaucoma. In specific embodiments of the invention, the alteration is: a
XX      change from GAG to AAG at codon 50 of the optineurin gene; an insertion
XX      of AG after codon 127; a change from CGG to CAG at codon 545; or a
XX      combination of one or more of these. These alterations are associated
XX      with glaucoma, and the presence of one or more of these alterations is a
XX      diagnostic for glaucoma. In another embodiment, the alteration is a
XX      change from ATG to AAG at codon 98. The presence of this alteration is a
XX      indicative of an increased risk of glaucoma, and is diagnostic of this
XX      increased risk. Other alterations include a change from CCC to GCC at
XX      codon 16, a change from CAG to CAC at codon 42, a change from GAA to GTA
XX      at codon 92, and a change from GAA to AAA at codon 322. Alterations
XX      include combinations of alterations such as combinations of alterations

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CC associated with glaucoma and those associated with an increased risk of  
CC glaucoma. Methods of detection, prognosis and diagnosis of the presence  
CC or absence of optineurin-associated glaucoma or of an optineurin-  
CC associated increased risk of glaucoma are described, in which a sample is  
CC tested for the presence of these gene sequence alterations or for  
CC alterations in the expression or activity of the optineurin protein. Also  
CC described are methods of therapy of glaucoma, including gene therapy  
CC methods.

XX SQ Sequence 2077 BP; 682 A; 431 C; 566 G; 398 T; 0 U; 0 Other;

Query Match		99.98;	Score 2075.4;	DB 12;	Length 2077;
Best Local Similarity		99.98;	Pred. No. 0;		
Matches 2076;		Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1	ATCCCGTCTGGGAGTTCTCTCCAGCGGCACGATCCGAGGAAACAGTGCACCTTGAGCGA	60		
Db	1	ATCCCGTCTGGGAGTTCTCTCCAGCGGCACGATCCGAGGAAACAGTGCACCTTGAGCGA	60		
Qy	61	AGCCAAGCCGGCGGCGAGGTGGCTTTGATAGCTGGTGGCCACTTCTGGCCTTGGGA	120		
Db	61	AGCCAAGCCGGCGGCGAGGTGGCTTTGATAGCTGGTGGCCACTTCTGGCCTTGGGA	120		
Qy	121	TGAGCCGTACGCCCTCTGTAAACCCAACTTCTCACCTTTGAAACAGCTGCTGGTTGAGC	180		
Db	121	TGAGCCGTACGCCCTCTGTAAACCCAACTTCTCACCTTTGAAACAGCTGCTGGTTGAGC	180		
Qy	181	ATTAATGAAGATTAGTCAGTGACAGGCTGTGTGCTGAGTCCGCACATAGAGAAATCAA	240		
Db	181	ATTAATGAAGATTAGTCAGTGACAGGCTGTGTGCTGAGTCCGCACATAGAGAAATCAA	240		
Qy	241	AAATGTCCAAAATGTAACTCGAGAGAAAGTGGCAACTTTTGGAGTGACTTTTCCACAGG	300		
Db	241	AAATGTCCAAAATGTAACTCGAGAGAAAGTGGCAACTTTTGGAGTGACTTTTCCACAGG	300		
Qy	301	AACCTTGTCAATGTCCCATCAACCTCTCAGCTGGCTCAGTGAAGAGAGACAGCCCCAG	360		
Db	301	AACCTTGTCAATGTCCCATCAACCTCTCAGCTGGCTCAGTGAAGAGAGACAGCCCCAG	360		
Qy	361	TGAAGCACAGGAAATGGACCCGCCACCTGGGCCACCCAAACCTGGACACGTTTACCCC	420		
Db	361	TGAAGCACAGGAAATGGACCCGCCACCTGGGCCACCCAAACCTGGACACGTTTACCCC	420		
Qy	421	GGAGGAGCTCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCCACAGCTGGAAGAAGC	480		
Db	421	GGAGGAGCTCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCCACAGCTGGAAGAAGC	480		
Qy	481	CATGAAGCTAAATCAAGCCATGAAGGGAGATTGAGGAGCTTTGGCCCTGGACAGA	540		
Db	481	CATGAAGCTAAATCAAGCCATGAAGGGAGATTGAGGAGCTTTGGCCCTGGACAGA	540		
Qy	541	GAACACAGAGGAAGAGCCAGTTTTTTTGAGATACAGAGCAAGAGCAAGAGCGTCT	600		
Db	541	GAACACAGAGGAAGAGCCAGTTTTTTTGAGATACAGAGCAAGAGCAAGAGCGTCT	600		
Qy	601	AATGGCCTTCAGTCATGAGAAATGAGAAATGGAAGGAGAGCTTTGGAAAACTAAAGGGA	660		
Db	601	AATGGCCTTCAGTCATGAGAAATGAGAAATGGAAGGAGAGCTTTGGAAAACTAAAGGGA	660		
Qy	661	ATCAGAAAGGTCACTGAGAACCCCACTGATGACTCCAGGCTTCCAGGCGCCGAAAGCGGA	720		
Db	661	ATCAGAAAGGTCACTGAGAACCCCACTGATGACTCCAGGCTTCCAGGCGCCGAAAGCGGA	720		
Qy	721	GCAGGAAGAGGACCACTCAGGACCCAGGTGGTGGCTACAGGACAGAGAGGACACCT	780		
Db	721	GCAGGAAGAGGACCACTCAGGACCCAGGTGGTGGCTACAGGACAGAGAGGACACCT	780		
Qy	781	GTGGGCACTCGTCTCTGAACTGACGCTCAAGCTGAACTCCAGCGGCTCTCAGAGATTTC	840		
Db	781	GTGGGCACTCGTCTCTGAACTGACGCTCAAGCTGAACTCCAGCGGCTCTCAGAGATTTC	840		
Qy	841	CTTTGTGAAATTAGGATGGCTGAAGAGAGAGAGAGGATCAGTAAAAAGAAATCAAGCA	900		
Db					

841	CTTTGTGAAATTAGGATGGCTGAAGAGAGAGAGAGGTCAGTAAAAAGAAATCAAGCA	900
901	TAGTCTCGGCCCCACGAGAACAGTCTCCACTGCACGGCAATGTCTAAATATAGGAGCAG	960
901	TAGTCTCGGCCCCACGAGAACAGTCTCCACTGCACGGCAATGTCTAAATATAGGAGCAG	960
961	ATCTGACAGATGGGGCCAAAGAAATTAATTGAAACATGAGGAGTTAACTGTGAGCAGCTCT	1020
961	ATCTGACAGATGGGGCCAAAGAAATTAATTGAAACATGAGGAGTTAACTGTGAGCAGCTCT	1020
1021	GCTTGCCCTAAGGAAGGGNATCAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGAGGC	1080
1021	GCTTGCCCTAAGGAAGGGNATCAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGAGGC	1080
1081	CAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCA	1140
1081	CAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCA	1140
1141	GACAGAGGGAGCACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTGGAAG	1200
1141	GACAGAGGGAGCACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTGGAAG	1200
1201	CGAAGTGGAAAGCACTGAACTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCA	1260
1201	CGAAGTGGAAAGCACTGAACTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCA	1260
1261	TACAAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGGTGTGAGGCCCT	1320
1261	TACAAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGGTGTGAGGCCCT	1320
1321	TGAAGGAAAAATTTCTGCAATTCATCAGAGTTGAAATGAAAGCAAGAGCTTGTATTATAC	1380
1321	TGAAGGAAAAATTTCTGCAATTCATCAGAGTTGAAATGAAAGCAAGAGCTTGTATTATAC	1380
1381	TAAACAAAAGTTAGAGCTACAGTGAAGAGATGCTATCAGAAATCAAAATGGAACAGGC	1440
1381	TAAACAAAAGTTAGAGCTACAGTGAAGAGATGCTATCAGAAATCAAAATGGAACAGGC	1440
1441	TAAACACAGAGGATGAAGAGTCCAAATTAATGCTGCTACAGATGACACACAAAGCTTCT	1500
1441	TAAACACAGAGGATGAAGAGTCCAAATTAATGCTGCTACAGATGACACACAAAGCTTCT	1500
1501	TCAAGAACATAATTAATGCAATGAAAACAATTTGAGGAACTAAACAAAGAAAGAGTCAAGAA	1560
1501	TCAAGAACATAATTAATGCAATGAAAACAATTTGAGGAACTAAACAAAGAAAGAGTCAAGAA	1560
1561	AGTGGACAGGCGAGTCTGAAAGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCT	1620
1561	AGTGGACAGGCGAGTCTGAAAGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCT	1620
1621	GGCTTCCAAACAGCTGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT	1680
1621	GGCTTCCAAACAGCTGCAATGGAATGGAATGGAATGGAATGGAATGGAATGGAATGGAAT	1680
1681	CCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTATGC	1740
1681	CCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTATGC	1740
1741	TGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGAGCAACTGGCAATGAGCTGGC	1800
1741	TGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGAGCAACTGGCAATGAGCTGGC	1800
1801	AGTTCTGCTGAAAGAGATGATGCTTTTGAAGACGAGGAGCGGCTCTGATGAGAT	1860
1801	AGTTCTGCTGAAAGAGATGATGCTTTTGAAGACGAGGAGCGGCTCTGATGAGAT	1860
1861	GCAGAGTCTCTATGGGGCGAGAACAGTGAATGCTGACCTGACAGAGGCTTACCTGTTCAAAG	1920
1861	GCAGAGTCTCTATGGGGCGAGAACAGTGAATGCTGACCTGACAGAGGCTTACCTGTTCAAAG	1920
1921	AGGAGCTGAGGACAGGAGCTGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA	1980
1921	AGGAGCTGAGGACAGGAGCTGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA	1980

QY 1981 GTGTGGAGAGGTTCTGCGTCGACATAGACACAGTTACAGATTCACTGATGATGATCATCAT 2040  
 |||||  
 Db 1981 GTGTGGAGAGGTTCTGCGTCGACATAGACACAGTTACAGATTCACTGATGATGATCATCAT 2040  
 |||||  
 QY 2041 TTAAGTGTGATGATATCACTCCCAAACTGTTGGT 2077  
 |||||  
 Db 2041 TTAAGTGTGATGATATCACTCCCAAACTGTTGGT 2077  
 |||||

## RESULT 3

AED20542

ID AED20542 standard; DNA; 2077 BP.

XX

AC AED20542;

XX

DT 01-DEC-2005 (first entry)

XX

DE Optineurin (OPTN) gene.

XX

KW ds; SNP; single nucleotide polymorphism; glaucoma; ophthalmological;

XX

KW ocular disease; Optineurin; OPTN; diagnostic; SNP detection.

XX

OS Homo sapiens.

XX

PN WO2005090602-A2.

XX

PD 29-SEP-2005.

XX

PF 18-MAR-2005; 2005WO-JP005601.

XX

PR 18-MAR-2004; 2004US-0553986P.

XX

PR 27-AUG-2004; 2004US-0604704P.

XX

PR 07-SEP-2004; 2004US-0607359P.

XX

PA (SUCA-) SUCAMPO AG.

XX

PI Mashima Y;

XX

PI WPI; 2005-659148/67.

XX

DR New set of genetic polymorphisms associated with optic neuropathy, useful

XX

PT for diagnosing or predicting susceptibility to optic neuropathy, e.g.

XX

PT glaucoma or Leber's disease.

XX

PS Example 6; Page 67-68; 150pp; English.

XX

XX The invention relates to a set of genetic polymorphisms associated with  
 CC optic neuropathy, which comprises at least one polymorphism selected  
 CC from: (1) AAG to AAT substitution at codon 198 of the Endothelin-1 gene  
 CC (lys198Asn); (2) -1370T-G polymorphism of the Endothelin-1 gene promoter  
 CC region; (3) A138 insertion/deletion (A138I/D) polymorphism in exon 1 of  
 CC the Endothelin-1 gene; (4) \*70C-G polymorphism in 3' non-coding region of  
 CC the Endothelin receptor A gene; (5) +1222C-T polymorphism of the  
 CC Endothelin Receptor A gene; (6) CAC to CAT substitution at codon 323 in  
 CC exon 6 of the Endothelin Receptor A gene (His323His); (7) -231A-G  
 CC polymorphism of the Endothelin Receptor A gene promoter region; (8) CTG  
 CC to CTA substitution at codon 277 in exon 4 of the Endothelin receptor B  
 CC gene; (9) 9099C-A polymorphism of the Mitochondrial gene; (10) 9101T-G  
 CC polymorphism of the Mitochondrial gene; (11) 9101T-C polymorphism of the  
 CC Mitochondrial gene; (12) 9804G-A polymorphism of the Mitochondrial gene;  
 CC (13) 11778G-A polymorphism of the Mitochondrial gene; (14) -713T-G  
 CC polymorphism of the Angiotensin II type 1 receptor gene promoter region;  
 CC (16) 3123C-A polymorphism of the Angiotensin II type 2 receptor gene;  
 CC (25) CAA to CGA substitution at codon 192 of the Paraoxonase 1 gene;  
 CC (Gln192Arg); (26) TTG to ATG substitution at codon 55 of the Paraoxonase  
 CC 1 gene (Ileu55Met); (27) CGG to CAG substitution at codon 144 of the  
 CC Noelin 2 gene (Arg144Gln); (32) GGA to CGA substitution at codon 389 of  
 CC the sbgr;1 adrenergic receptor gene (Gly389Arg); (35) 1105T-C  
 CC polymorphism of the Myocilin gene (Phe369Leu); (36) 412G-A polymorphism  
 CC of the Optineurin gene; (37) 1402C-T polymorphism of the E-Selectin gene;  
 CC (38) the combination of polymorphisms of -8570T of the Tumor necrosis  
 CC factor a gene promoter region and 412G-A of the Optineurin gene; (39) the

CC combination of polymorphisms of -863C-A of the Tumor necrosis factor a  
 CC gene promoter region and 603T-A of the Optineurin gene; (40) CGC to CCC  
 CC substitution at codon 72 of the TP53 gene (Arg72Pro); (41) TAC to CAC  
 CC substitution at codon 113 of the Microsomal 25 epoxide hydrolase gene  
 CC (Tyr113His); (42) -110A-C polymorphism of the Heatshock protein 70-1 gene  
 CC promoter region; (43) -338C-A polymorphism of the Endothelin converting  
 CC enzyme gene promoter region; (44) -670A-G polymorphism of the CD95 gene  
 CC promoter region; (45) AAG to AAA substitution at codon 119 of the  
 CC Microsomal epoxide hydrolase 1 gene (Lys119Lys); (47) GGA to AGA  
 CC substitution at codon 16 of the dbgr;2 adrenergic receptor gene  
 CC (Gly16Arg); or (48) CAA to GAA substitution at codon 27 of the dbgr;2  
 CC adrenergic receptor gene (Gln27Glu). Also included are: (1) a method of  
 CC diagnosing or predicting susceptibility to optic neuropathy in a human  
 CC subject; (2) a kit for diagnosing or predicting susceptibility to optic  
 CC neuropathy, e.g. glaucoma or Leber's disease, in a human subject  
 CC comprising primer set and/or probe suitable for determining genotype in  
 CC respect of a set of genetic polymorphisms comprising at least one genetic  
 CC polymorphism selected from those given above; (3) an isolated  
 CC polynucleotide comprising: (a) a segment of a fully defined 360 bp  
 CC sequence, where the segment comprises at least 90 continuous nucleotide,  
 CC and the at least 90 continuous nucleotide includes position 9099 of the  
 CC sequence, and where position 9099 of the sequence is A, or an isolated  
 CC polynucleotide which is entirely complementary to the above segment; (b)  
 CC a segment of a fully defined 300 bp sequence, where the segment comprises  
 CC at least 90 continuous nucleotide, and the at least 90 continuous  
 CC nucleotide includes codon 369, which is corresponding to the underlined  
 CC nucleotides of the sequence, and where codon 369 is substituted so that  
 CC it codes for Leu, or an isolated polynucleotide which is entirely  
 CC complementary to the above segment; or (c) a segment of a fully defined  
 CC 540 bp sequence, where the segment comprises at least 90 continuous  
 CC nucleotide, and the at least 90 continuous nucleotide includes codon 144,  
 CC which is corresponding to the underlined nucleotides of the sequence, and  
 CC where codon 144 is substituted such that it codes for Gln, or an  
 CC isolated, polynucleotide which is entirely complementary to the above  
 CC segment; (4) treating glaucoma in a patient who has an abnormality in the  
 CC Myocilin gene; and (5) predicting the response of a subject to the  
 CC treatment with a drug. The genetic polymorphisms are useful for  
 CC diagnosing or predicting susceptibility to optic neuropathy, e.g.  
 CC glaucoma or Leber's disease, and for predicting the response of a subject  
 CC to treatment with a drug. Suppressing the expression of abnormal Myocilin  
 CC genes by RNA interference is useful for treating glaucoma in a subject  
 CC with an abnormality in the Myocilin genes. The present sequence  
 CC represents a segment of the Optineurin (OPTN) gene which contains an  
 CC optic neuropathy associated single nucleotide polymorphism (SNP).

XX Sequence 2077 BP; 682 A; 431 C; 566 G; 398 T; 0 U; 0 Other;

Query Match 99.9%; Score 2075.4; DB 14; Length 2077;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2076; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATCCCGGTGCGGAGTTCTCTCCAGGCGGCACGATGCCAGGAAACAGTCACTGAGCGCA 60

Db 1 ATCCCGGTGCGGAGTTCTCTCCAGGCGGCACGATGCCAGGAAACAGTCACTGAGCGCA 60

QY 61 AGCCAAAGCCGCGGCGAGGTGGCTTTGATAGCTGGTGGTGGCCACTTCTGCGCCTTGA 120

Db 61 AGCCAAAGCCGCGGCGAGGTGGCTTTGATAGCTGGTGGTGGCCACTTCTGCGCCTTGA 120

QY 121 TCAGCGGTACGCTCTGTAAACCCCACTTCCTCACCTTTGAAACAGCTCGCTGGTTTCAGC 180

Db 121 TCAGCGGTACGCTCTGTAAACCCCACTTCCTCACCTTTGAAACAGCTCGCTGGTTTCAGC 180

QY 181 ATTAATGAAGATTAGTTCAGTGACGAGCCCTGGTGTGCTGAGTCCGCAATAGAAGATCAA 240

Db 181 ATTAATGAAGATTAGTTCAGTGACGAGCCCTGGTGTGCTGAGTCCGCAATAGAAGATCAA 240

QY 241 AAATGTCAAAATGTAATCTGGAGAGAAAGTGGCAACTTTTGGAGTGCATTTTCCACAGG 300

Db 241 AAATGTCAAAATGTAATCTGGAGAGAAAGTGGCAACTTTTGGAGTGCATTTTCCACAGG 300

QY 301 AACTTCTGCAATGTCCCATCAACCTTCTCAGTGCCTCACTGAAAAAGGAGACAGCCCCAG 360

XX |||||

Db 301 AACTTCTCAATGTCCCATCAACCTCTCAGCTGCTCTACTGAAAGAGGAGACAGCCCGAG 360  
Qy 361 TGAAGCACAGAAATGGAACCCCGCCACCTGGCCCGCCCAACCTGGACAGCTTTTACCCC 420  
Db 361 TGAAGCACAGAAATGGAACCCCGCCACCTGGCCCGCCCAACCTGGACAGCTTTTACCCC 420  
Qy 421 GGAGAGCTGTCGACGAGATGAAGAGCTCTCTGACCAAGAACACACAGCTGAAAGAAC 480  
Db 421 GGAGAGCTGTCGACGAGATGAAGAGCTCTCTGACCGAGAACACACAGCTGAAAGAAC 480  
Qy 481 CATGAAGCTAAATTAATCAAGCCATGAAAGGGAGATTTGAGAGCTTTTGGGCTCGACAGA 540  
Db 481 CATGAAGCTAAATTAATCAAGCCATGAAAGGGAGATTTGAGAGCTTTTGGGCTCGACAGA 540  
Qy 541 GAAACAGAGAAAGAACCCAGTTTTTTTGAGATACAGAGCAAGAAAGAAAGAGCGTCT 600  
Db 541 GAAACAGAGAAAGAACCCAGTTTTTTTGAGATACAGAGCAAGAAAGAAAGAGCGTCT 600  
Qy 601 AATGGCCCTTGAATCATGAGATGAGAAATGAAAGGAGAGCTTGGAAACTTAAAGGGAA 660  
Db 601 AATGGCCCTTGAATCATGAGATGAGAAATGAAAGGAGAGCTTGGAAACTTAAAGGGAA 660  
Qy 661 ATCAGAAAGGTCTATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGA 720  
Db 661 ATCAGAAAGGTCTATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGA 720  
Qy 721 GCAGGAAAGGACCCAGCTCAGGACCCAGGTGGTGAAGCTCAAGCAGAGAGGCGACACT 780  
Db 721 GCAGGAAAGGACCCAGCTCAGGACCCAGGTGGTGAAGCTCAAGCAGAGAGGCGACACT 780  
Qy 781 GTTGGGCAATCGTGTCTGAATCGAGCTCAAGCTGAACTCCAGGGCTTCTCAGAAGATTC 840  
Db 781 GTTGGGCAATCGTGTCTGAATCGAGCTCAAGCTGAACTCCAGGGCTTCTCAGAAGATTC 840  
Qy 841 CTTTGTGTAATTAGGATGCTGAGAGAGAGAGAGAGAGGTGAGTAAAGAAATCAAGCA 900  
Db 841 CTTTGTGTAATTAGGATGCTGAGAGAGAGAGAGAGGTGAGTAAAGAAATCAAGCA 900  
Qy 901 TAGTCTCTGGGCCCAACAGAAACAGTCTCCACTGGCAGGGCAATGTCTAAATATAGGAGCAG 960  
Db 901 TAGTCTCTGGGCCCAACAGAAACAGTCTCCACTGGCAGGGCAATGTCTAAATATAGGAGCAG 960  
Qy 961 ATCTGCAGATGGGGCCCAAGAAATTAATTCGAACATGAGAGCTTAACCTGTGAGCCAGCTCT 1020  
Db 961 ATCTGCAGATGGGGCCCAAGAAATTAATTCGAACATGAGAGCTTAACCTGTGAGCCAGCTCT 1020  
Qy 1021 GCTGTGCTTAAGGAGAGGGAATCAGAGGTGGAGAGACTTGAAGTTCACCTCAAGAGGC 1080  
Db 1021 GCTGTGCTTAAGGAGAGGGAATCAGAGGTGGAGAGACTTGAAGTTCACCTCAAGAGGC 1080  
Qy 1081 CAAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGATTCGAACCCA 1140  
Db 1081 CAAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGATTCGAACCCA 1140  
Qy 1141 GACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCGGAGACTGTGTGAAG 1200  
Db 1141 GACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCGGAGACTGTGTGAAG 1200  
Qy 1201 CGAAGTGAAGCACTGAACTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCA 1260  
Db 1201 CGAAGTGAAGCACTGAACTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCA 1260  
Qy 1261 TACAAACTCAGCGAGCTCAGCTAATGAAGAGAGACTTCAAGAAAGTGTGAGGCCCT 1320  
Db 1261 TACAAACTCAGCGAGCTCAGCTAATGAAGAGAGACTTCAAGAAAGTGTGAGGCCCT 1320  
Qy 1321 TGAAGGAAATTTCTGCAATTCATCAGAGTTGAAATGAAAGCAAGAGCTTGTATTATAC 1380  
Db 1321 TGAAGGAAATTTCTGCAATTCATCAGAGTTGAAATGAAAGCAAGAGCTTGTATTATAC 1380  
Qy 1381 TAACAAAAGTTAGAGCTACAAGTGAAGAGCACTGCTATCAGAAATCAAAATGGAACAGGC 1440  
Db 1381 TAACAAAAGTTAGAGCTACAAGTGAAGAGCACTGCTATCAGAAATCAAAATGGAACAGGC 1440

Qy 1441 TAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGCTTCT 1500  
Db 1441 TAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGCTTCT 1500  
Qy 1501 TCAAGAACATAATATGCTGATGAAACAAATTTAGGAACTAAACAGAAAGAGTCAAGAAA 1560  
Db 1501 TCAAGAACATAATATGCTGATGAAACAAATTTAGGAACTAAACAGAAAGAGTCAAGAAA 1560  
Qy 1561 AGTGGACAGGGCAGTCTGAAAGGAACCTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCT 1620  
Db 1561 AGTGGACAGGGCAGTCTGAAAGGAACCTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCT 1620  
Qy 1621 GGCTTCCAAACAGCTGCAAAATGGAATGGAATGAAGCAAAACCATTCGCAAGCAGGAAGAGGA 1680  
Db 1621 GGCTTCCAAACAGCTGCAAAATGGAATGGAATGAAGCAAAACCATTCGCAAGCAGGAAGAGGA 1680  
Qy 1681 CCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGATTTACTGTCTGATTTTCATGC 1740  
Db 1681 CCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGATTTACTGTCTGATTTTCATGC 1740  
Qy 1741 TGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCAATTCGAGCTGGC 1800  
Db 1741 TGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCAATTCGAGCTGGC 1800  
Qy 1801 AGTTCTGCTGAAAGAGAAATGATGCTTTTCCGAAGACGAGGAGGAGCTCTTGATGGAGAT 1860  
Db 1801 AGTTCTGCTGAAAGAGAAATGATGCTTTTCCGAAGACGAGGAGGAGCTCTTGATGGAGAT 1860  
Qy 1861 GCAGAGTCGTCTGGGGCGAGAAACAAAGTGAATCTGACACAGAGGCTTACCTTGTTCAAAG 1920  
Db 1861 GCAGAGTCGTCTGGGGCGAGAAACAAAGTGAATCTGACACAGAGGCTTACCTTGTTCAAAG 1920  
Qy 1921 AGGAGCTGAGGACAGGAGCTGGGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA 1980  
Db 1921 AGGAGCTGAGGACAGGAGCTGGGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA 1980  
Qy 1981 GTGTGGAGAGTTCTGCTGACATAGACAGCTTACAGATTCACGTGATGATTCATCAT 2040  
Db 1981 GTGTGGAGAGTTCTGCTGACATAGACAGCTTACAGATTCACGTGATGATTCATCAT 2040  
Qy 2041 TTAAGTGTGATGATATCACCTCCCAAAACCTGTTGGT 2077  
Db 2041 TTAAGTGTGATGATATCACCTCCCAAAACCTGTTGGT 2077

## RESULT 4

ADL15031

ID ADL15031 standard; DNA; 2139 BP.

XX AC ADL15031;

XX XX

DT 06-MAY-2004 (first entry)

XX Human FIP2 DNA for cancer treatment.

XX ds; gene; cytostatic; gene therapy; binding moiety; medicine; imaging;

XX diagnosis; prognosis; mantle cell lymphoma; cancer.

XX Homo sapiens.

XX WO2003068268-A2.

XX 21-AUG-2003.

XX 13-FEB-2003; 2003WO-EP001461.

XX 14-FEB-2002; 2002GB-00003480.

XX 29-JUN-2002; 2002GB-00015095.

XX (BIOI-) BIOINVENT INT AB.

XX Ek S, Borrebaeck CAK, Ehinger M;

PI





QY	840	CTTTTGTGAAATTAGGATGGCTGAAAGAGAAAGCAGAGGGTCAGTAAAGAAATCAAGC	899	1920	GAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCCGATTCAATTCCTGCCCA	1979
Db	856	CTTTTGTGAAATTAGGATGGCTGAAAGAGAAAGCAGAGGGTCAGTAAAGAAATCAAGC	915	1936	GAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCCGATTCAATTCCTGCCCA	1995
QY	900	ATAGTCTGGGCCACGAGAAACAGTCTCACTGGCAGCGCATTGCTAAATATAGGACA	959	1980	AGTGTGGAGAGGTTCTGCTGCATAGACACGCTTACAGATTACCGTGTGGATTGCATCA	2039
Db	916	ATAGTCTGGGGTCCAGAGAACAGTCTCCACTGGCAGCGCATGTCTCATATAGGAGA	975	1996	AGTGTGGAGAGGTTCTGCTGCATAGACACGCTTACAGATTACCGTGTGGATTGCATCA	2055
QY	960	GATCTCAGATGGGGCCAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAGCTCC	1019	2040	TTTAAAGTGTGATGATPACACCTCCCTCCCAAACTGTTGGT	2077
Db	976	GATCTCAGATGGGGCCAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAGCTCC	1035	2056	TTTAAAGTGTGATGATPACACCTCCCTCCCAAACTGTTGGT	2093
QY	1020	TGCTGTGCCCTAAGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACCTCAAGGAG	1079	RESULT 6		
Db	1036	TGCTGTGCCCTAAGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACCTCAAGGAG	1095	ID	ADR24267	
QY	1080	CMAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTCTTGAGATTGAACCC	1139	XX	ADR24267;	
Db	1096	CCAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTCTTGAGATTGAACCC	1155	XX	21-OCT-2004 (first entry)	
QY	1140	AGACAGAGGGAGCAGACAGAGAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAA	1199	XX	Breast cancer prognosis marker #128.	
Db	1156	AGACAGAGGGAGCAGACAGAGAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAA	1215	XX	ds; breast cancer; prognosis; gene expression; diagnosis.	
QY	1200	GCAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTC	1259	OS	Homo sapiens.	
Db	1216	GCAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTC	1275	XX	WO2004065545-A2.	
QY	1260	ATCAAACTCAGCGAAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTCAAGGCC	1319	PD	05-AUG-2004.	
Db	1276	ATCAAACTCAGCGAAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTCAAGGCC	1335	PF	15-JAN-2004; 2004WO-US001100.	
QY	1320	TTCAAGAGGAAATCTGCAATTCATCGAGTTGAATGAAGCAAGAGCTTGTGTTATA	1379	PR	15-JAN-2003; 2003US-00342887.	
Db	1336	TTCAAGAGGAAATCTGCAATTCATCGAGTTGAATGAAGCAAGAGCTTGTGTTATC	1395	XX	(ROSE-) ROSETTA INPHARMATICS LLC.	
QY	1380	CTAACAAAAGTTAGAGCTACAAAGTGAAGCACTGCTATCAGAAATCAAAATGGAAACAG	1439	PA	(NECA-) NETHERLANDS CANCER INST.	
Db	1396	CTAACAAAAGTTAGAGCTACAAAGTGAAGCACTGCTATCAGAAATCAAAATGGAAACAG	1455	XX	Van't Veer LJ, He Y;	
QY	1440	CTAAACAGAGGATGAAAGTCAAAATTAATCTGTGCTACAGATGACACACAAAGCTTC	1499	XX	WPI; 2004-593473/57.	
Db	1456	CTAAACAGAGGATGAAAGTCAAAATTAATCTGTGCTACAGATGACACACAAAGCTTC	1515	XX	Classifying a breast cancer patient according to prognosis comprises	
QY	1500	TTCAAGAACATAATATGCTTGAACCAATTCAGGAATTAACAGAAAGAGTTCAGAAA	1559	PT	determining the similarity between the level of expression of each of	
Db	1516	TTCAAGAACATAATATGCTTGAACCAATTCAGGAATTAACAGAAAGAGTTCAGAAA	1575	PT	five genes in a cell sample taken from patient, to control levels.	
QY	1560	AAGTGGACAGGGCAGTGTCTGAAGGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTC	1619	XX	Disclosure; SEQ ID NO 128; 226pp; English.	
Db	1576	AAGTGGACAGGGCAGTGTCTGAAGGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTC	1635	CC	The invention relates to a method of classifying a breast cancer patient	
QY	1620	TGGCTTCAAACAGCTGCAATGGAATGAAGCAACCATTCGCAAGCAGAGAGAGG	1679	CC	according to prognosis by determining the similarity between the level of	
Db	1636	TGGCTTCAAACAGCTGCAATGGAATGAAGCAACCATTCGCAAGCAGAGAGAGG	1695	CC	expression of each of five genes for which markers are listed in the	
QY	1680	ACCTGGAAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTCTGATTTTCATG	1739	CC	specification, in a cell sample taken from the breast cancer patient, to	
Db	1696	ACCTGGAAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTCTGATTTTCATG	1755	CC	control levels of expression for each respective five genes to obtain a	
QY	1740	CTGAAAGAGCAGCGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCATTCAGCTGG	1799	CC	patient similarity value. The methods are useful for classifying a breast	
Db	1756	CTGAAAGAGCAGCGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCATTCAGCTGG	1815	CC	cancer patient according to prognosis. Kits and computer program products	
QY	1800	CAGTTCTGCTGAAGAGAAATGATGCTTTCGAAGCAGGAGCAGGCTTCATGAGAGA	1859	CC	are useful for data analysis using the diagnostic, prognostic and	
Db	1816	CAGTTCTGCTGAAGAGAAATGATGCTTTCGAAGCAGGAGCAGGCTTCATGAGAGA	1875	CC	statistical methods of the invention. This sequence corresponds to a	
QY	1860	TGCAGAGTCTGCTGAGGGCCAGAAACAGTGAATCTGACACAGCAGGCTTACCTTGTTCAAA	1919	CC	marker used in the method of the invention.	
Db	1876	TGCAGAGTCTGCTGAGGGCCAGAAACAGTGAATCTGACACAGCAGGCTTACCTTGTTCAAA	1935	XX	Sequence 2139 BP; 708 A; 446 C; 574 G; 411 T; 0 U; 0 Other;	
Query Match 99.0%; Score 2056.4; DB 13; Length 2139;						
Best Local Similarity 99.7%; Pred. No. 0;						
Matches 2071; Conservative 0; Mismatches 6; Indels 1; Gaps 1;						
QY	1	ATCCCCGGTCGGAGTTCTCTCCAGGGCGGCACATGCGGAGGAAACAGTGACCTGAGCGA	60	QY	1	ATCCCCGGTCGGAGTTCTCTCCAGGGCGGCACATGCGGAGGAAACAGTGACCTGAGCGA
Db	16	ATCCCCGGTCGGAGTTCTCTCCAGGGCGGCACATGCGGAGGAAACAGTGACCTGAGCGA	75	Db	16	ATCCCCGGTCGGAGTTCTCTCCAGGGCGGCACATGCGGAGGAAACAGTGACCTGAGCGA
QY	61	AGCCAAAGCCGGCGGAGGTGGCTTTGATAGCTGGTGGTGCACCTTCCTGGCCTTGGGA	120	QY	61	AGCCAAAGCCGGCGGAGGTGGCTTTGATAGCTGGTGGTGCACCTTCCTGGCCTTGGGA
Db	76	AGCCAAAGCCGGCGGAGGTGGCTTTGATAGCTGGTGGTGCACCTTCCTGGCCTTGGGA	135	Db	76	AGCCAAAGCCGGCGGAGGTGGCTTTGATAGCTGGTGGTGCACCTTCCTGGCCTTGGGA



Qy	121	TGAGCGGTACGGCTCTGTAAACCCAACTCTCTCACTTTTGAAACAGCTGCCTGGTTTCAGC	181
Db	136	TGAGCGGTACGCGCTCTGTAAACCCAACTCTCTCACTTTTGAAACAGCTGCCTGGTTTCAGC	195
Qy	181	ATTAAATGAAGATTAGTCTAGTCACAGGCGCTGTGTCTCAGTCCGACATAGAAGNATCAA	240
Db	196	ATTAAATGAAGATTAGTCTAGTCACAGGCGCTGTGTCTCAGTCCGACATAGAAGNATCAA	255
Qy	241	AAATGTCCAAAATGTAACTGGAGAGAAAGTGGGCAACTTTT - GGAGTGTACTTTTCCACAG	299
Db	256	AAATGTCCAAAATGTAACTGGAGAGAAAGTGGGCAACTTTTGGGAGTGACTTTTCCACAG	315
Qy	300	GAACTTCTGCAATGTCCCATCAACTCTCTCAGCTGCCTCAGTGAAGAGAGACAGCCCA	359
Db	316	GAACTTCTGCAATGTCCCATCAACTCTCTCAGCTGCCTCAGTGAAGAGAGACAGCCCA	375
Qy	360	GTGAAAGCACAGGAAATGGACCCCCACCTCTGGCCACCCCAAACTCTGACAGCTTTACCC	419
Db	376	GTGAAAGCACAGGAAATGGACCCCCACCTCTGGCCACCCCAAACTCTGACAGCTTTACCC	435
Qy	420	CGGAGGAGCTGCTCGACGAGATGAAAGAGCTCCTTGACCAAGAACCCACAGCTGAAAGAAG	479
Db	436	CGGAGGAGCTGCTCGACGAGATGAAAGAGCTCCTTGACCGAGAACCCACAGCTGAAAGAAG	495
Qy	480	CCATGAAGCTAAATAATCAAGCCATGAAAGGAGATTGAGGAGCTTTTCGGCTCTGGACAG	539
Db	496	CCATGAAGCTAAATAATCAAGCCATGAAAGGAGATTGAGGAGCTTTTCGGCTCTGGACAG	555
Qy	540	AGAAACAGAGGAAGAACGCCAGTTTTTTTGAGATACAGAGCAAAAGNAGCAAAAGCGTCT	599
Db	556	AGAAACAGAGGAAGAACGCCAGTTTTTTTGAGATACAGAGCAAAAGNAGCAAAAGCGTCT	615
Qy	600	TAAATGGGCTTGAGTCAATGAGAAATGAGAAATTTGAAAGGAAGAGCTTTGGAAGGGA	659
Db	616	TAAATGGGCTTGAGTCAATGAGAAATTTGAAAGGAAGAGCTTTGGAAGGGA	675
Qy	660	AATCAGAAAGGTATCTGAGAACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAAGCGG	719
Db	676	AATCAGAAAGGTATCTGAGAACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAAGCGG	735
Qy	720	AGCAGGAAAGGACCACTCAGGACCCAGGTGGTGGCTTACAGCAGAGNAGGACAGACC	779
Db	736	AGCAGGAAAGGACCACTCAGGACCCAGGTGGTGGCTTACAGCAGAGNAGGACAGACC	795
Qy	780	TGTTGGGCGATCGTCTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGGTCTCTCAGAAGATT	839
Db	796	TGTTGGGCGATCGTCTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGGTCTCTCAGAAGATT	855
Qy	840	CTTTTGTGTAATTTAGGATGCTGAAGAGAGCAGAAAGGCTCAGTAAAAAGAAATCAAGC	899
Db	856	CTTTTGTGTAATTTAGGATGCTGAAGAGAGCAGAAAGGCTCAGTAAAAAGAAATCAAGC	915
Qy	900	ATAGTCTCTGGGCCCAACAGAACAGTCTCCACTGCGCAGCGCATTTGCTTAATATAGGAGCA	959
Db	916	ATAGTCTCTGGGTCCACAGAACAGTCTCCACTGCGCAGCGCATTTGCTCAGTATAGGAGGA	975
Qy	960	GATCTGCAGATGGGGCCAAAGAAATTTACTTTGAAACATGAGGAGTTAACTGTGAGCCAGCTCC	1019
Db	976	GATCTGCAGATGGGGCCAAAGAAATTTACTTTGAAACATGAGGAGTTAACTGTGAGCCAGCTCC	1035
Qy	1020	TGCTGTGCCTTAAGGGAAGGGGAATCAGAAAGGTGGAGAGACTTTGAAAGTTGCACTCAAGGAGG	1079
Db	1036	TGCTGTGCCTTAAGGGAAGGGGAATCAGAAAGGTGGAGAGACTTTGAAAGTTGCACTCAAGGAGG	1095
Qy	1080	CCAAGAAAGAGTTTCAGATTTTGAAAGAGAAACAAAGTAAATCGTTCGTAGATTGAAACCC	1139
Db	1096	CCAAGAAAGAGTTTCAGATTTTGAAAGAGAAACAAAGTAAATCGTTCGTAGATTGAAACCC	1155
Qy	1140	AGACAGAGGGGAGCACAGAGAAAGAGAAATGATGAAAGAGAAAGGCCCGGAGACTGTTGGA	1199
Db	1156	AGACAGAGGGGAGCACAGAGAAAGAGAAATGATGAAAGAGAAAGGCCCGGAGACTGTTGGA	1215
Qy	1200	GCGAAGTGGAGACACTGAACTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTC	1259

[illegible]

KW Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;  
KW immune system disorder; hypersensitivity; anaphylaxis;  
XX blood group incompatibility; ds; human.  
OS Homo sapiens.  
XX WO200280852-A2.  
XX 17-OCT-2002.  
XX 04-APR-2002; 2002WO-US010873.  
XX 04-APR-2001; 2001US-0281416P.  
XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.  
XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;  
XX WPI; 2003-075470/07.  
XX Novel isolated or purified polypeptide encoded by genes associated with  
PT intestinal epithelium or M cell development, differentiation or function,  
PT useful for treating autoimmune diseases and infectious diseases.  
XX Claim 1; SEQ ID NO 248; 152pp; English.  
XX The invention comprises DNA sequences which are associated with  
CC intestinal epithelium and Peyer's patch M cells. The DNA sequences of the  
CC invention are useful for assessing, modifying, modulating or regulating  
CC intestinal epithelium or M cell development. The DNA sequences of the  
CC invention are also useful in the treatment of: inflammatory bowel  
CC disease, glutenenteropathy, infectious diseases, autoimmune diseases  
CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's  
CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),  
CC diseases or disorders of the immune system, hypersensitivity,  
CC anaphylaxis, and blood group incompatibility. The present nucleic acid  
CC represents an intestinal epithelium/Peyer's patch M cell-associated DNA  
CC sequence of the invention. NOTE: The present sequence is not shown in the  
CC specification, but has been retrieved from the WIPO website.  
XX  
SQ Sequence 2108 BP; 686 A; 439 C; 573 G; 410 T; 0 U; 0 Other;

Query Match 98.9%; Score 2053.2; DB 10; Length 2108;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 2069; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

QY 1 ATCCCGTGGGAGTTCTCTCCAGGGGCGACGATCCGAGGAAACAGTGACCTGAGCGA 60  
DB 14 ATCCCGTGGGAGTTCTCTCCAGGGGCGACGATCCGAGGAAACAGTGACCTGAGCGA 73  
QY 61 AGCCAAAGCCGGGCGGAG-GTGTGGCTTTGATAGCTGGTGGTCCACTTCTCGGCTTGG 119  
DB 74 AGCCAAAGCCGGGCGGAGAGTGTGGCTTTGATAGCTGGTGGTCCACTTCTCGGCTTGG 133  
QY 120 ATGAGCGTACGGCTGTGTAACCCAACTTCTCACCCTTTGAAACAGCTGCCTGTTTAC 179  
DB 134 ATGAGCGTACGGCTGTGTAACCCAACTTCTCACCCTTTGAAACAGCTGCCTGTTTAC 193  
QY 180 CATTAATGAGATTAGTCAGTGACAGCCCTGGTGTGCTGAGTCGACATAGAGAATCA 239  
DB 194 CATTAATGAGATTAGTCAGTGACAGCCCTGGTGTGCTGAGTCGACATAGAGAATCA 253  
QY 240 AAAATGTCCAAAATGTAACGGAGAGAAAGTGGGCAACTTTTGGAGTGACTTTTCCACAG 299  
DB 254 AAAATGTCCAAAATGTAACGGAGAGAAAGTGGGCAACTTTTGGAGTGACTTTTCCACAG 313  
QY 300 GAATCTTGCAATGTCCCATCACTCTCAGCTGCCTCCTCAGTGAAGAGGAGCAGCCCCA 359  
DB 314 GAATCTTGCAATGTCCCATCACTCTCAGCTGCCTCCTCAGTGAAGAGGAGCAGCCCCA 373  
QY 360 GTGAAAGCAGGAAATGGACCCCTGAGCCCAACCCCACTGGACACCTGTTACCC 419  
DB 374 GTGAAAGCAGGAAATGGACCCCTGAGCCCAACCCCACTGGACACCTGTTACCC 433

QY 420 CGGAGGAGCTGCTGCAGCAGATGAAAGAGCTCTCTGACCAAGAACCAACAGCTGAAAGAAG 479  
DB 434 CGGAGGAGCTGCTGCAGCAGATGAAAGAGCTCTCTGACCAAGAACCAACAGCTGAAAGAAG 493  
QY 480 CCATGAAGCTAAATTAATCAAGCCATGAAAGGAGAGTTTTCGAGAGCTTTTCGAGAGCTG 539  
DB 494 CCATGAAGCTAAATTAATCAAGCCATGAAAGGAGAGTTTTCGAGAGCTTTTCGAGAGCTG 553  
QY 540 AGAAAACAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 599  
DB 554 AGAAAACAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 613  
QY 600 TAAATGCTTGAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 659  
DB 614 TAAATGCTTGAAGTCAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 673  
QY 660 AATCAGAAAGGTCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 719  
DB 674 AATCAGAAAGGTCATCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 733  
QY 720 AGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 779  
DB 734 AGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 793  
QY 780 TGTGGGCAATCGTGTCTGAACTGAGCTCAAGCTGAACTCCAGCGGCTCTCAGAGATT 839  
DB 794 TGTGGGCAATCGTGTCTGAACTGAGCTCAAGCTGAACTCCAGCGGCTCTCAGAGATT 853  
QY 840 CTTTGTGTAATTAAGGATGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 899  
DB 854 CTTTGTGTAATTAAGGATGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 913  
QY 900 ATAGTCTGGGGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959  
DB 914 ATAGTCTGGGGCCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 973  
QY 960 GATCTGAGATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1019  
DB 974 GATCTGAGATGGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1033  
QY 1020 TGTGTGCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1079  
DB 1034 TGTGTGCTTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1093  
QY 1080 CCAAGAGAAAGAGTTTCAGATTTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1139  
DB 1094 CCAAGAGAAAGAGTTTCAGATTTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153  
QY 1140 AGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1199  
DB 1154 AGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1213  
QY 1200 GCGAGTGAAGCAGCTGAACTCCAGGTCACATCTCTGTTTAAAGAGAGCTTCAAGAGGCTC 1259  
DB 1214 GCGAGTGAAGCAGCTGAACTCCAGGTCACATCTCTGTTTAAAGAGAGCTTCAAGAGGCTC 1273  
QY 1260 ATACAAAACTCAGCGAGGAGCTGAGCTAATGAAGAGAGAGCTTCAAGAAAAAGTGTCAAGCCC 1319  
DB 1274 ATACAAAACTCAGCGAGGAGCTGAGCTAATGAAGAGAGAGCTTCAAGAAAAAGTGTCAAGCCC 1333  
QY 1320 TTGAAAGGAAAAATTCCTGCAATTCATCAGAGTTGAATGAAGAGAGAGCTTGTGTTATA 1379  
DB 1334 TTGAAAGGAAAAATTCCTGCAATTCATCAGAGTTGAATGAAGAGAGAGCTTGTGTTATC 1393  
QY 1380 CTAACAAAAAGTTAGAGCTACAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1439  
DB 1394 CTAACAAAAAGTTAGAGCTACAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1453  
QY 1440 CTAACAAAAAGTTAGAGCTACAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1499  
DB 1454 CTAACAAAAAGTTAGAGCTACAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1513

QY 1500 TTCAAGAACATAATAATCATTTGAAACAAATTTGGGAACTAACAGAAAGAGTCAGAAA 1559  
Db 1514 TTCAAGAACATAATAATCATTTGAAACAAATTTGGGAACTAACAGAAAGAGTCAGAAA 1573  
QY 1560 AAGTGGACAGGCGAGTCTGAAGCACTGAGTGAAGAACTGGAACCTGCGACAGAGGCTC 1619  
Db 1574 AAGTGGACAGGCGAGTCTGAAGCACTGAGTGAAGAACTGGAACCTGCGACAGAGGCTC 1633  
QY 1620 TGGCTTCCAAACAGCTGCAAAATGATGAATGAAGCAAAACCATTTGCCAAGCAGGAAGG 1679  
Db 1634 TGGCTTCCAAACAGCTGCAAAATGATGAATGAAGCAAAACCATTTGCCAAGCAGGAAGG 1693  
QY 1680 ACCTGGAAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1739  
Db 1694 ACCTGGAAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1753  
QY 1740 CTGAAAGAGCAGCAGAGAGAAAATTCATGAGGAAGAGGACCACTGGCATTGCGAGCTGG 1799  
Db 1754 CTGAAAGAGCAGCAGAGAGAAAATTCATGAGGAAGAGGACCACTGGCATTGCGAGCTGG 1813  
QY 1800 CAGTTCTCTGAAAGAGAAATGATGCTTTTCGAAGACGGGAGGCGAGCTCCTTGATGGAGA 1859  
Db 1814 CAGTTCTCTGAAAGAGAAATGATGCTTTTCGAAGACGGGAGGCGAGCTCCTTGATGGAGA 1873  
QY 1860 TGCAGAGTCGTATGGGCGAGAAACAGTGACTCTGACACGAGCGCTTACCTTGTCAAA 1919  
Db 1874 TGCAGAGTCGTATGGGCGAGAAACAGTGACTCTGACACGAGCGCTTACCTTGTCAAA 1933  
QY 1920 GAGCAGCTGAGCAGGAGCTGGGCGCAACAGCGGAATATTCGCAATTCATCTGCCCCA 1979  
Db 1934 GAGCAGCTGAGCAGGAGCTGGGCGCAACAGCGGAATATTCGCAATTCATCTGCCCCA 1993  
QY 1980 AGTGTGGAGAGTTCTGCTGACATAGACACGTTTACAGATTTCAGTGTGATGATGATCA 2039  
Db 1994 AGTGTGGAGAGTTCTGCTGACATAGACACGTTTACAGATTTCAGTGTGATGATGATCA 2053  
QY 2040 TTTAAGTGTGATGATATCACCTCCCAAACTGTGTGT 2077  
Db 2054 TTTAAGTGTGATGATATCACCTCCCAAACTGTGTGT 2091

RESULT 8

ADP23349  
ID ADP23349 standard; cDNA; 3904 BP.

AC ADP23349;

XX 18-NOV-2004 (first entry)

DE PRO polypeptide encoding cDNA SEQ ID NO:443.

XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
KW immunosuppressive; osteopathic; antidiabetic; dermatological;  
KW antipruritic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
KW gene therapy; immune system.

XX Unidentified.

XX WO2004041170-A2.

XX 21-MAY-2004.

XX 30-OCT-2003; 2003WO-US034312.

XX 01-NOV-2002; 2002US-0423394P.

XX (GETH ) GENENTECH INC.

XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
PI Wu TD;

XX WPI; 2004-419628/39.

DR P-PSDB; ADP23350.

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Query Match

Best Local Similarity

Matches 2075; Conservative

Score 98.8%;

Pred. No. 0;

Mismatches 1;

Indels 2;

Gaps 2;

Length 3904;

DB 13;

Score 2052.4;

Score 99.9%;

Pred. No. 0;

Mismatches 0;

Indels 1;

Gaps 2;

Length 3904;

DB 13;

Score 2052.4;

Score 99.9%;

Pred. No. 0;

Mismatches 0;

Indels 1;

Gaps 2;

Length 3904;

DB 13;

Score 2052.4;

Score 99.9%;

Pred. No. 0;

Mismatches 0;

Indels 1;

Gaps 2;

Length 3904;

DB 13;

Score 2052.4;

Score 99.9%;

New PRO polypeptides and polynucleotides, useful for treating e.g. erythematosis, rheumatoid arthritis, diabetes mellitus, immune-mediated renal disease, or demyelinating diseases of the central or peripheral nervous system.

Claim 1; SEQ ID NO 443; 2940pp; English.

The invention relates to a novel isolated nucleic acid and the PRO polypeptide encoded by it. A protein of the invention has antiinflammatory, antiarthritic, antirheumatic, immunosuppressive, osteopathic, antidiabetic, dermatological, antipruritic, antiallergic, antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide of the invention may have a use in gene therapy. The PRO polypeptide, its agonist, antagonist, or antibody that specifically binds to the polypeptide is useful for treating an immune related disorder such as systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an idiopathic inflammatory myopathy, Sjogren's syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, a demyelinating disease of the central or peripheral nervous system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome, a chronic inflammatory demyelinating polynuropathy, a hepatobiliary disease, infectious or autoimmune chronic active hepatitis, primary biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis, inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's disease, an autoimmune or immune-mediated skin disease, a bullous skin disease, erythema multiforme, contact dermatitis, psoriasis, an allergic disease, asthma, allergic rhinitis, atopic dermatitis, food hypersensitivity, urticaria, an immunologic disease of the lung, eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity pneumonitis, a transplantation associated disease, graft rejection or graft-versus-host disease. The present sequence encodes a PRO protein of the invention.

Sequence 3904 BP; 1154 A; 674 C; 821 G; 928 T; 0 U; 327 Other;

QY	480	CCATGAAGCTAAATAATCAAGCCATCAAAAGGGAGATTTGAGGAGCTTTTCGGCTCGACAG	539
Db	495	CCATGAAGCTAAATAATCAAGCCATCAAAAGGGAGATTTGAGGAGCTTTTCGGCTCGACAG	554
QY	540	AGAAACAGAGGAGAACCCAGTCTTTTTCAGATACAGAGCAAGCAAGCAAGCAAGCGTC	599
Db	555	AGAAACAGAGGAGAACCCAGTCTTTTTCAGATACAGAGCAAGCAAGCAAGCAAGCGTC	614
QY	600	TAATGSCCTTGAGTCATGAGAAATGAGAAATGGAAGGAAGAGCTTGGAAAACTAAAAAGGGA	659
Db	615	TAATGSCCTTGAGTCATGAGAAATGAGAAATGGAAGGAAGAGCTTGGAAAACTAAAAAGGGA	674
QY	660	AATCAGAAAGGTCATCTGAGGACCCCACTGATGATCCAGGCTCCAGGGCCGGAAGCGG	719
Db	675	AATCAGAAAGGTCATCTGAGGACCCCACTGATGATCCAGGCTCCAGGGCCGGAAGCGG	734
QY	720	AGCAGAAAGGACACAGCTCAGAACCCAGGTGGTGAAGGCTTACAGCAGAGNAGGCAGACC	779
Db	735	AGCAGAAAGGACACAGCTCAGAACCCAGGTGGTGAAGGCTTACAGCAGAGNAGGCAGACC	794
QY	780	TGTTGGGCATCGTGTCTGAACCTCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATT	839
Db	795	TGTTGGGCATCGTGTCTGAACCTCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATT	854
QY	840	CCTTTGTTGAAATTAGATGGCTGAAAGGAAGCAGAGGGTCAGTAAAGAAATCAAGC	899
Db	855	CCTTTGTTGAAATTAGATGGCTGAAAGGAAGCAGAGGGTCAGTAAAGAAATCAAGC	914
QY	900	ATAGTCCTGGGCCACGAGNACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGGACCA	959
Db	915	ATAGTCCTGGGCCACGAGNACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGGACCA	974
QY	960	GATCTCGAGATGGGCCCAAGAAATTACTTCGAAATCAGGAGTTAACTGTGAGCCAGCTCC	1019
Db	975	GATCTCGAGATGGGCCCAAGAAATTACTTCGAAATCAGGAGTTAACTGTGAGCCAGCTCC	1034
QY	1020	TGCTGTGCTTAAGGGAAGGGAATCAGAAAGTGAGAGACTTGAAGTTGCACCTCAAGGAGG	1079
Db	1035	TGCTGTGCTTAAGGGAAGGGAATCAGAAAGTGAGAGACTTGAAGTTGCACCTCAAGGAGG	1094
QY	1080	CCAAAGAGAGTTTCAGATTTTGAAGAAACAAAGTAATCTGTTCTGAGATTGAACCC	1139
Db	1095	CCAAAGAGAGTTTCAGATTTTGAAGAAACAAAGTAATCTGTTCTGAGATTGAACCC	1154
QY	1140	AGACAGAGGGGACACAGAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTGTGGAA	1199
Db	1155	AGACAGAGGGGACACAGAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTGTGGAA	1214
QY	1200	GCGAAGTGGAGACCTGAACCTCAAGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTC	1259
Db	1215	GCGAAGTGGAGACCTGAACCTCAAGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTC	1274
QY	1260	ATACAAAACCTCAGGAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGTCAAGCCCC	1319
Db	1275	ATACAAAACCTCAGGAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGTCAAGCCCC	1334
QY	1320	TTCAAAAGGAAAAATTTCTGCAATTCCTCAGAGTTGAATGAAAAAGCAAGCTTTGTTTATA	1379
Db	1335	TTGAAAGGAAAAATTTCTGCAATTCCTCAGAGTTGAATGAAAAAGCAAGCTTTGTTTATA	1394
QY	1380	CTAACAAAAAGTTAGAGCTCAAGTGGAAGAGATGCTATCAGAAATCAAAATGGAACAGG	1439
Db	1395	CTAACAAAAAGTTAGAGCTCAAGTGGAAGAGATGCTATCAGAAATCAAAATGGAACAGG	1454
QY	1440	CTAAACAGAGGATGAAAGTCCAAATTAACCTGCTTACAGATGACACACAAAGCTTC	1499
Db	1455	CTAAACAGAGGATGAAAGTCCAAATTAACCTGCTTACAGATGACACACAAAGCTTC	1514
QY	1500	TTCAAGAACATAATAATGCTTTGAAAAACAATGAGGAACTTAACAAGAAAAAGAGTCAGAAA	1559
Db	1515	TTCAAGAACATAATAATGCTTTGAAAAACAATGAGGAACTTAACAAGAAAAAGAGTCAGAAA	1574
QY	1560	AAAGTGACAGGGCAGTCTGAGGAACTGAGTGAAAACTGGCACTGGCAGAGNAGGCTC	1619
Db	1575	AAAGTGACAGGGCAGTCTGAGGAACTGAGTGAAAACTGGCACTGGCAGAGNAGGCTC	1634
QY	1620	TGGCTTCACAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCATTTGCCAAGCAGGAAGAGG	1679
Db	1635	TGGCTTCACAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCATTTGCCAAGCAGGAAGAGG	1694
QY	1680	ACCTGGAACCAATGATACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGATTTTTCATG	1739
Db	1695	ACCTGGAACCAATGATACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGATTTTTCATG	1754
QY	1740	CTGAAGAGCAGCAGAGAGAAAAATTCATGAGAAAAAGAGCAACTGGCATTTGCAGCTGG	1799
Db	1755	CTGAAGAGCAGCAGAGAGAAAAATTCATGAGAAAAAGAGCAACTGGCATTTGCAGCTGG	1814
QY	1800	CAGTTCTGCTGAAAGAGAAATGATGCTTTCGAAAGACGAGAGGAGGAGTCTTGTATGGAGA	1859
Db	1815	CAGTTCTGCTGAAAGAGAAATGATGCTTTCGAAAGACGAGAGGAGGAGTCTTGTATGGAGA	1874
QY	1860	TCGAGAGTCGTATGGGGCGAGAAACAAAGTGAATCTTGACACAGAGGCTTACCTTGTTCAAA	1919
Db	1875	TCGAGAGTCGTATGGGGCGAGAAACAAAGTGAATCTTGACACAGAGGCTTACCTTGTTCAAA	1934
QY	1920	GAGGAGCTGAGCAGAGGAGTGGCGCAACAGCGGAATATTCGATTCTTCCTGCCCCA	1979
Db	1935	GAGGAGCTGAGCAGAGGAGTGGCGCAACAGCGGAATATTCGATTCTTCCTGCCCCA	1994
QY	1980	AGTGTGGAGAGGTTCTGCTGACATAGACACGTTACAGATTACGTTGATGGATTGCATCA	2039
Db	1995	AGTGTGGAGAGGTTCTGCTGACATAGACACGTTACAGATTACGTTGATGGATTGCATCA	2054
QY	2040	TTTAAAGTGTGATGATATACCTCCCAAAAACTGTTGGT	2077
Db	2055	TTTAAAGTGTGATGATATACCTCCCAAAAACTGTTGGT	2092
RESULT 9			
AAH57391			
ID	AAH57391 standard; cdNA; 3454 BP.		
XX	AAH57391;		
AC	10-SEP-2001 (first entry)		
DT	Human skeletal muscle cell specific cDNA sequence SEQ ID NO:231.		
XX	Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;		
XX	liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;		
KW	metabolic disease; developmental disease; cystostatic; immunomodulatory;		
KW	neuroprotective; gene therapy; cancer; immunopathology; neuropathology.		
OS	Homo sapiens.		
XX	WO200132927-A2.		
PN	10-MAY-2001.		
XX	02-NOV-2000; 2000WO-US030396.		
XX	04-NOV-1999; 99US-0163508P.		
PR	(INCY-) INCYTE GENOMICS INC.		
XX	Sornasse T, Seilhamer JJ, Watson GA;		
PI	WPI; 2001-291057/30.		
XX	New cell and tissue specific polynucleotides useful for diagnosis, is		
PT	prognosis or monitoring of treatments for disorders where the gene is		
PT	associated with a cancer, immunopathology or neuropathology.		
XX	Claim 1; Page 159-160; 327pp; English.		
PS			

xx AAH57161 to AAH5756 represent cell and tissue specific polynucleotide  
cc sequences (I). (I) can have cytostatic, immunomodulatory and  
cc neuroprotective activities, and can be used in gene therapy. (I) and  
cc proteins (II) encoded by then are used in high throughput screening  
cc assays to select DNA molecules, RNA molecules, peptide nucleic acids,  
cc minetics, peptides, proteins, agonists, antagonists, antibodies or their  
cc fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical  
cc agents. Expression of (I) in a sample indicates the differentiation of  
cc embryonic stem cells into a tissue selected from brain, heart, kidney,  
cc liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used  
cc to produce an expression profile that defines a metabolic or  
cc developmental process, treatment, condition, disease or disorder. The  
cc gene profile can be used for diagnosis, prognosis or monitoring of  
cc treatments and for investigating a predisposition to a disorder where the  
cc gene is associated with a cancer, immunopathology or neuropathology  
xx  
SQ Sequence 3454 BP; 1094 A; 725 C; 794 G; 841 T; 0 U; 0 Other;

Query Match 95.2%; Score 1976.8; DB 4; Length 3454;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 2000; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

Qy 1 ATCCCGGTCGGAGTTCTCCAGCGCGCACGATGCCGAGAAACAGTGAACCTTGAGCGA 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 16 ATCCCGGTCGGAGTTCTCCAGCGCGCACGATGCCGAGAAACAGTGAACCTTGAGCGA 75  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 61 AGCCAAAGCCGGCGGAGTGTGCTTTGATAGCTGGTGGTGCACATTCCTGGCCTTGGGA 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 76 AGCCAAAGCCGGCGGAGTGTGCTTTGATAGCTGGTGGTGCACATTCCTGGCCTTGGGA 135  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 121 TGAGCCGTACGCCCTCTGPAACCCCAACTTCTCACTTTGAAACAGCTGCCGTGTTGAGC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 136 TGAGCCGTACGCCCTCTGPAACCCCAACTTCTCACTTTGAAACAGCTGCCGTGTTGAGC 195  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 181 ATTAATGAAGATTAGTCAGTGACAGGCTGTGTGCTGAGTCCCGACATAGAGAATCAA 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 196 ATTAATGAAGATTAGTCAGTGACAGGCTGTGTGCTGAGTCCCGACATAGAGAATCAA 255  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 241 AAATGTCCAAATGTAACTGGAGAGAAAGTGGGCAACTTTT - GGAGTGACTTTTCCACAG 299  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 256 AAATGTCCAAATGTAACTGGAGAGAAAGTGGGCAACTTTTGGAGTGACTTTTCCACAG 315  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 300 GAACTTCTGCAATCTCCATCAACCTCTCAGCTGCCCTCACTGAAAGAGGACAGCCCA 359  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 316 GAACTTCTGCAATCTCCATCAACCTCTCAGCTGCCCTCACTGAAAGAGGACAGCCCA 375  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 360 GTGAAGCACAGGAATGGACCCCTCCAGCTGCCCTCACTGAAAGAGGACAGCCCA 418  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 376 GTGAAGCACAGGAATGGACCCCTCCAGCTGCCCTCACTGAAAGAGGACAGCCCA 435  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 419 CCGGAGGAGCTGTGTCAGCAGATGAAGAGCTCTGACCAAGAACCCAGCTGAAAGAA 478  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 436 CCGGAGGAGCTGTGTCAGCAGATGAAGAGCTCTGACCGAGAACCCAGCTGAAAGAA 495  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 479 GCCATGAAGCTTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTGGCCTTGACA 538  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 496 GCCATGAAGCTTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTGGCCTTGACA 555  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 539 GAGAAACAGAAAGGAACCGCAGTTTTTTTGAAGATACAGAGCAAGAAAGAGAGCGT 598  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 556 GAGAAACAGAAAGGAACCGCAGTTTTTTTGAAGATACAGAGCAAGAAAGAGAGCGT 615  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 599 CTAATGCCCTTGTGTCATGAGATGAGAAATTTGAGGAGAGCTTTGAAACCTTAAAGGG 658  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 616 CTAATGCCCTTGTGTCATGAGATGAGAAATTTGAGGAGAGCTTTGAAACCTTAAAGGG 675  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 659 AAATCAGAAAGGTCACTCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGCGCGAAGCG 718  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 676 AAATCAGAAAGGTCACTCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGCGCGAAGCG 735  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Qy 719 GAGCAGAAAGGACAGTCTCAGAACCCAGTGGTGGGTGTACAGCAGAGAAAGGCAGAC 778  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 736 GAGCAGAAAGGACCAGCTCAGGACCCAGGTGTGAGGCTTACAAGCAGAGAGGACGAC 795  
Qy 779 CTGTTGGGCATCTGTCGTAACCTCAGCTCAAGCTGAACCTCCAGCGCTCTCTCAGAGAT 838  
Db 796 CTGTTGGGCATCTGTCGTAACCTCAGCTCAAGCTGAACCTCCAGCGCTCTCTCAGAGAT 855  
Qy 839 TCCTTTGTTGAAATTAGGATGGCTGGAAGGAGAAACAGAGGGTCAGTAAAGAAATCAAG 898  
Db 856 TCCTTTGTTGAAATTAGGATGGCTGGAAGGAGAAACAGAGGGTCAGTAAAGAAATCAAG 915  
Qy 899 CATAGTCTGGGCCCCCAGAGAACAGTCTCAGCTGGCAGCGCATTTCTAAATATAGGAGC 958  
Db 916 CATAGTCTGGGCCCCCAGAGAACAGTCTCAGCTGGCAGCGCATTTCTAAATATAGGAGC 975  
Qy 959 AGATCTCAGATGGGCGCAAGAAATTAATTCGAAACATCAGGAGTTAACTGTGAGCAGCTC 1018  
Db 976 AGATCTCAGATGGGCGCAAGAAATTAATTCGAAACATCAGGAGTTAACTGTGAGCAGCTC 1035  
Qy 1019 CTGCTGTGCTTAAGGGAAGGGAATCAGAGGTGGAGAGACTTGAAGTTGCACTCAAGAGG 1078  
Db 1036 CTGCTGTGCTTAAGGGAAGGGAATCAGAGGTGGAGAGACTTGAAGTTGCACTCAAGAGG 1095  
Qy 1079 GCCAAAGAAAGAGTTTTCAGATTTTGAAGAAAGAAACAAAGTAATCTCTCTGAGATTGAAACC 1138  
Db 1096 GCCAAAGAAAGAGTTTTCAGATTTTGAAGAAAGAAACAAAGTAATCTCTCTGAGATTGAAACC 1155  
Qy 1139 CAGACAGAGGGAGCACAGAGAAAGAAATGATGAAGAGAAAGCCCGGAGACTGTTTGA 1198  
Db 1156 CAGACAGAGGGAGCACAGAGAAAGAAATGATGAAGAGAAAGCCCGGAGACTGTTTGA 1215  
Qy 1199 AGCGAAGTGAAGCAGCTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCT 1258  
Db 1216 AGCGAAGTGAAGCAGCTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCT 1275  
Qy 1259 CATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCC 1318  
Db 1276 CATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCC 1335  
Qy 1319 CTTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTGTTGTTAT 1378  
Db 1336 CTTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTGTTGTTAT 1395  
Qy 1379 ACTAACAAAAGTTAGAGCTACAAGTGAAGAGCATGCTATCAGAAAATCAAAAATGGAACAG 1438  
Db 1396 ACTAACAAAAGTTAGAGCTACAAGTGAAGAGCATGCTATCAGAAAATCAAAAATGGAACAG 1455  
Qy 1439 GCTTAAACAGAGATGAAGAGTCCAAATTAATCTGTGCTACAGATGACACACAAGAGCTT 1498  
Db 1456 GCTTAAACAGAGATGAAGAGTCCAAATTAATCTGTGCTACAGATGACACACAAGAGCTT 1515  
Qy 1499 CTTCAAGAACATTAATGCAATTTGAAACCAATTTGAGGAACTTAACAGAAAAGAGTCAAGAA 1558  
Db 1516 CTTCAAGAACATTAATGCAATTTGAAACCAATTTGAGGAACTTAACAGAAAAGAGTCAAGAA 1575  
Qy 1559 AAAGTGGACAGGCGCAGTGTGTAAGAGAACTCAGTGAAGAAATCGGAACTGGCAGAGAGGCT 1618  
Db 1576 AAAGTGGACAGGCGCAGTGTGTAAGAGAACTCAGTGAAGAAATCGGAACTGGCAGAGAGGCT 1635  
Qy 1619 CTGGCTTCCAAAACAGCTGCAAAATGGATGAAATGAAAGCAAAACCAATTCGCAAGCAGGAAGAG 1678  
Db 1636 CTGGCTTCCAAAACAGCTGCAAAATGGATGAAATGAAAGCAAAACCAATTCGCAAGCAGGAAGAG 1695  
Qy 1679 GACCTGGAAACCATGATGACCATCTCAGGCTCAGATGGAGTTTACTGTTCTGATTTTCAT 1738  
Db 1696 GACCTGGAAACCATGATGACCATCTCAGGCTCAGATGGAGTTTACTGTTCTGATTTTCAT 1755  
Qy 1739 GCTGAAAGAGCAGCGAGAGAGAGAAATTTCAAGAGAAAGAGAGCAACTGGCATTTGCAGCTG 1798  
Db 1756 GCTGAAAGAGCAGCGAGAGAGAGAAATTTCAAGAGAAAGAGAGCAACTGGCATTTGCAGCTG 1815  
Qy 1799 GCAGTTCTGCTGAAAGAGAGATGATGCTTTTGAAGACGAGGCGGAGCAGTCTTGTATGGAG 1858  
Db 1816 GCAGTTCTGCTGAAAGAGAGATGATGCTTTTGAAGACGAGGCGGAGCAGTCTTGTATGGAG 1875

QY 1859 ATGCAGAGTCGTATGCGGCGAGACAAAGTGACTCTGACCAGCAGGCTTACCTTGTTCAA 1918  
Db 1876 ATGCAGAGTCGTATGCGGCGAGACAAAGTGACTCTGACCAGCAGGCTTACCTTGTTCAA 1935  
QY 1919 AGAGGAGCTGAGACAGGAGCTGGCGGCAACAGCGGAATATCCGATTATTCCTGCCCC 1978  
Db 1936 AGAGGAGCTGAGACAGGAGCTGGCGGCAACAGCGGAATATTCGGAATATTCCTGCCCC 1995  
QY 1979 AAGTGTGGAGAGTCTTGCTGCTGAC 2002  
Db 1996 AAGTGTGGAGAGTCTTGCTGCTGCC 2019

RESULT 10  
ACF03998  
ID ACF03998 standard; cDNA; 2008 BP.  
XX  
AC ACF03998;  
XX  
DT 23-SEP-2003 (first entry)  
XX  
DE Human optineurin isoform 3 encoding cDNA SEQ ID NO:5.  
XX  
KW Human; optineurin; OPTN; chromosome 10; 10p14; glaucoma; ophthalmic;  
KW gene therapy; gene; ss.  
XX  
OS Homo sapiens.

XX  
FH Key Location/Qualifiers  
FT CDS 242..1975  
FT FT /\*tag= a  
FT FT /product= "optineurin isoform 3"

XX W02003056037-A1.

XX 10-JUL-2003.

XX 18-DEC-2002; 2002WO-US041116.

XX 24-DEC-2001; 2001US-0344754P.

XX 30-JAN-2002; 2002US-00060981.

XX 28-FEB-2002; 2002US-00090118.

XX 25-OCT-2002; 2002US-00281454.

XX (UYCO-) UNIV CONNECTICUT.

XX (SGEO-) ST GEORGES ENTERPRISES LTD.

XX Sarfarazi M, Rezaie T, Child AH;

XX WPI; 2003-598273/56.

XX P-PSDB; ABR82079.

XX Claim 1; Page 76-79; 83pp; English.

XX The present invention describes a method (M1) for diagnosing the presence  
CC or absence of optineurin-associated glaucoma or an optineurin-associated  
CC increased risk of glaucoma in an individual comprising detecting the  
CC presence or absence of an alteration in expression, composition or  
CC activity of an optineurin nucleic acid or polypeptide, which is  
CC indicative of the presence or absence, respectively, of the optineurin-  
CC associated glaucoma. Optineurin has ophthalmic activity and can be used  
CC in gene therapy. Optineurin therapeutic agents can be used for the  
CC manufacture of a medicament for the treatment of glaucoma or of an  
CC increased risk for glaucoma. Human optineurin is located on chromosome  
CC 10, more specifically to 10p14. The present sequence encodes human  
CC optineurin isoform 3, which is used in the exemplification of the present  
CC invention

XX SQ Sequence 2008 BP; 656 A; 421 C; 549 G; 382 T; 0 U; 0 Other;  
Query Match 92.8%; Score 1927.4; DB 9; Length 2008;  
Best Local Similarity 96.6%; Pred. No. 0;  
Matches 2007; Conservative 0; Mismatches 1; Indels 69; Gaps 1;  
QY 1 ATCCCGGTGGAGTTCCTCCAGGCGGCACGATCCGAGGAAACAGTCACTTACCTGAGCGA 60  
Db 1 ATCCCGGTGGAGTTCCTCCAGGCGGCACGATCCGAGGAAACAGTCACTTACCTGAGCGA 60  
QY 61 AGCCAAGCGGCGCGAGGTGGCTTTGATAGCTGGTGCCTTCTCTGCGCTTGA 120  
Db 61 AGCCAAGCGGCGCGAGGTGGCTTTGATAGCTGGTGCCTTCTCTGCGCTTGA 120  
QY 121 TGAGCGGTACGCTCTGTAAACCCCAACTTCTCACCTTTGAAACAGCTCGCTGGTTGAGC 180  
Db 121 TGAGCGGTACGCTCTGTAAACCCCAACTTCTCACCTTTGAAACAGCTCGCTGGTTGAGC 180  
QY 181 ATTAATGAAGATTAGTCAGTGACAGGCTGTGTGTGCTGAGTCGGCACAATAGAAGATCAA 240  
Db 181 ATTAATGAAGATTAGTCAGTGACAGGCTGTGTGTGCTGAGTCGGCACAATAGAAGATCAA 240  
QY 241 AATGTCCAAAATGTAACTGGAGAGAAAGTGGGCAACTTTTGGAGTGACTTTTCCACAGG 300  
Db 231 -----G 231  
QY 301 AACTTCTGCAATGTCCCATCAACTCTCTCAGCTGCCTCACTGAAAGAGGACAGCCCCAG 360  
Db 232 AACTTCTGCAATGTCCCATCAACTCTCTCAGCTGCCTCACTGAAAGAGGACAGCCCCAG 291  
QY 361 TGAAGCACAGGAAATGGACCCCCCACTGGGCCCAACCAACCTTGGACAGCTTTTACCCC 420  
Db 292 TGAAGCACAGGAAATGGACCCCCCACTGGGCCCAACCAACCTTGGACAGCTTTTACCCC 351  
QY 421 GGAGGAGCTGCTGCAGCAGATGAAGAGCTCTTGACCAAGAACACACAGCTGAAGAGC 480  
Db 352 GGAGGAGCTGCTGCAGCAGATGAAGAGCTCTTGACCAAGAACACACAGCTGAAGAGC 411  
QY 481 CATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCCGCTTGGACAGA 540  
Db 412 CATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCCGCTTGGACAGA 471  
QY 541 GAAACAGAGGAGAAAGCCAGTTCCTGAGATACAGAGCAAGAGCAAGAGAGCTCT 600  
Db 472 GAAACAGAGGAGAAAGCCAGTTCCTGAGATACAGAGCAAGAGCAAGAGAGCTCT 531  
QY 601 AATGGCTTTGAGTCATGAGAATGAGAAATTGAAGGAAGAGCTTTGGAATACTAAAGGGA 660  
Db 532 AATGGCTTTGAGTCATGAGAATGAGAAATTGAAGGAAGAGCTTTGGAATACTAAAGGGA 591  
QY 661 ATCAGAAAGGTTCATCTGAGGACCCCACTGATGATCCAGGCTTTCCAGGCGCCGAAGCGGA 720  
Db 592 ATCAGAAAGGTTCATCTGAGGACCCCACTGATGATCCAGGCTTTCCAGGCGCCGAAGCGGA 651  
QY 721 GCAGGAAAAGGACCACTCAGGACCCAGTGGTGAGGCTTACAGCAGAGAGAGCAGACCT 780  
Db 652 GCAGGAAAAGGACCACTCAGGACCCAGTGGTGAGGCTTACAGCAGAGAGAGCAGACCT 711  
QY 781 GTTGGCATCGTCTGTAAGCTCAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 840  
Db 712 GTTGGCATCGTCTGTAAGCTCAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAGCT 771  
QY 841 CTTTGTGAAATTTAGGATGGCTGAGGAGAGAGAGGAGGAGTCAAGTAAAGAAATCAAGCA 900  
Db 772 CTTTGTGAAATTTAGGATGGCTGAGGAGAGAGAGGAGGAGTCAAGTAAAGAAATCAAGCA 831  
QY 901 TAGTCTGGGCCCAAGAGAACAGTCTCCACTGCGACGGCAATTTCTTAAATATATAGGAGCAG 960  
Db 832 TAGTCTGGGCCCAAGAGAACAGTCTCCACTGCGACGGCAATTTCTTAAATATATAGGAGCAG 891  
QY 961 ATCTGCAGATGGGGCCCAAGAAATTAATTCGAAACATGAGGAGTAACTGTGAGCCAGCTCT 1020

Db 892 ATCTCCAGATGGGGCCAAAGAATTACTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCCT 951  
QY 1021 GCTGTGCCCTAAGGGGAAGGAATCAGAAGGTGAGAGACTTGAAGTTGCACTCAAGGAGGC 1080  
Db 952 GCTGTGCCCTAAGGGGAAGGAATCAGAAGGTGAGAGACTTGAAGTTGCACTCAAGGAGGC 1011  
QY 1081 CAAGAAGAGGTTTCAGATTGTTGAAAAGAAAACAGTAATCGTTCTGAGATTGAACCCCA 1140  
Db 1012 CAAGAAGAGGTTTCAGATTGTTGAAAAGAAAACAGTAATCGTTCTGAGATTGAACCCCA 1071  
QY 1141 GACAGAGGGGACACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTGGGAAG 1200  
Db 1072 GACAGAGGGGACACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTGGGAAG 1131  
QY 1201 CGAAGTGAAGACTGAACCTCCAGGTGCATCTCTGTTTAAAGAGCTTCAAGAGGCTCA 1260  
Db 1132 CGAAGTGAAGACTGAACCTCCAGGTGCATCTCTGTTTAAAGAGCTTCAAGAGGCTCA 1191  
QY 1261 TACAAAACCTCAGCGAAGCTGAGCTAAATCAAGAAGAGACTTCAAGAAAGTCTCAGGCCT 1320  
Db 1192 TACAAAACCTCAGCGAAGCTGAGCTAAATCAAGAAGAGACTTCAAGAAAGTCTCAGGCCT 1251  
QY 1321 TGAAGGAAAATTTCTGCAATTTCCATCAGAGTTGAAATGAAAAGCAAGAGCTTGTTTATAC 1380  
Db 1252 TGAAGGAAAATTTCTGCAATTTCCATCAGAGTTGAAATGAAAAGCAAGAGCTTGTTTATAC 1311  
QY 1381 TAACAAAAAGTTAGAGCTTACAAGTGGAAAGCATCTATCAGAAATCAAAATGGAACAGGC 1440  
Db 1312 TAACAAAAAGTTAGAGCTTACAAGTGGAAAGCATCTATCAGAAATCAAAATGGAACAGGC 1371  
QY 1441 TAAACACAGAGATGAAAAGTCCAAATTAACGTGCTACAGATGACACACAAAGCTTCT 1500  
Db 1372 TAAACACAGAGATGAAAAGTCCAAATTAACGTGCTACAGATGACACACAAAGCTTCT 1431  
QY 1501 TCAAGAAACATAAATTAATGATTGAAAACAAATTTGAGGAACTAACAGAAAAGAGTCAGAAAA 1560  
Db 1432 TCAAGAAACATAAATTAATGATTGAAAACAAATTTGAGGAACTAACAGAAAAGAGTCAGAAAA 1491  
QY 1561 AGTGGACAGGCGAGTGTGGAAGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCT 1620  
Db 1492 AGTGGACAGGCGAGTGTGGAAGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCT 1551  
QY 1621 GGCTTCCAAACAGCTGCAATGGAATGAAATGAAGCAAAACCTTCCCAAGCGAGGAAGGA 1680  
Db 1552 GGCTTCCAAACAGCTGCAATGGAATGAAATGAAGCAAAACCTTCCCAAGCGAGGAAGGA 1611  
QY 1681 CCTGGAACCATGATACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGC 1740  
Db 1612 CCTGGAACCATGATACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGC 1671  
QY 1741 TGAAGAGACGCGAGAGAGAAAATTCATGAGGAAAAGGAGCAACTGGCAATTGCGAGCTGGC 1800  
Db 1672 TGAAGAGACGCGAGAGAGAAAATTCATGAGGAAAAGGAGCAACTGGCAATTGCGAGCTGGC 1731  
QY 1801 AGTTCTCTGAAAGAGATGATGCTTTCGAAAGCGGAGGAGGAGGCTTTCATGATGAGAT 1860  
Db 1732 AGTTCTCTGAAAGAGATGATGCTTTCGAAAGCGGAGGAGGAGGCTTTCATGATGAGAT 1791  
QY 1861 GCAGAGTCGTATGGGCGAGAAACAAGTGAAGTCTGACACAGGCTTACCTGTTTCAAG 1920  
Db 1792 GCAGAGTCGTATGGGCGAGAAACAAGTGAAGTCTGACACAGGCTTACCTGTTTCAAG 1851  
QY 1921 AGGAGCTGAGGACAGGAGCTGGGCGCAACAGCGGAATATTTCCGATTCATTTCTGCCCCAA 1980  
Db 1852 AGGAGCTGAGGACAGGAGCTGGGCGCAACAGCGGAATATTTCCGATTCATTTCTGCCCCAA 1911  
QY 1981 GTGTGGAGAGGTTCTGCTGACATAGACAGCTTACAGATTCACGTGATGATTCATCAT 2040  
Db 1912 GTGTGGAGAGGTTCTGCTGACATAGACAGCTTACAGATTCACGTGATGATTCATCAT 1971  
QY 2041 TTAAGTGTGATGATATCACTCCCAAACTGTTGGT 2077  
Db 1972 TTAAGTGTGATGATATCACTCCCAAACTGTTGGT 2008

## RESULT 11

ADO43187 ID ADO43187 standard; cDNA; 2008 BP.

XX ADO43187;

XX AC ADO43187;

XX DT 29-JUL-2004 (first entry)

XX Human optineurin isoform 3 cDNA, associated with glaucoma.

XX Human; optineurin; glaucoma; diagnosis; gene therapy; ophthalmological;

XX KW gene; chromosome 10p14; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 242..1975

XX FT /\*tag= a

XX FT /product= "Human optineurin isoform 3"

XX WO2004039312-A2.

XX FN 13-MAY-2004.

XX XX 26-JUN-2003; 2003WO-US020165.

XX XX 25-OCT-2002; 2002US-00281457.

XX XX (UYCO-) UNIV CONNECTICUT.

XX PA (SGEO-) ST GEORGES ENTERPRISES LTD.

XX XX Sarfarazi M, Rezaie T, Child AH;

XX PI WPI; 2004-376046/35.

XX DR P-PSDB; ADO43188.

XX DR GENBANK; AF420373.

XX XX New optineurin nucleic acids and polypeptides having sequence

XX PT alterations, which indicates the presence of an optineurin-associated

XX PT (risk of) glaucoma, useful for detecting or diagnosing glaucoma, e.g.

XX PT primary open angle glaucoma.

XX XX Claim 1; SEQ ID NO 5; 110pp; English.

XX CC The present sequence is that of cDNA encoding isoform 3 of human

XX CC optineurin (optic neuropathy inducing protein). Mutation of the

XX CC optineurin gene on chromosome 10 is associated with primary open angle

XX CC glaucoma. In specific embodiments of the invention, the alteration is

XX CC numbering according to optineurin isoform 1 cDNA ADO43183): a change

XX CC from GAG to AAG at codon 50 of the optineurin gene; an insertion of AG

XX CC after codon 127; a change from CGG to CAG at codon 545; or a combination

XX CC of one or more of these. These alterations are associated with glaucoma,

XX CC and the presence of one or more of these alterations is diagnostic for

XX CC glaucoma. In another embodiment, the alteration is a change from ATG to

XX CC AAG at codon 98. The presence of this alteration is indicative of an

XX CC increased risk of glaucoma, and is diagnostic of this increased risk.

XX CC Other alterations include a change from CCC to GCC at codon 16, a change

XX CC from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, and a

XX CC change from GAA to AAA at codon 322. Alterations include combinations of

XX CC alterations such as combinations of alterations associated with glaucoma

XX CC and those associated with an increased risk of glaucoma. Methods of

XX CC detection, prognosis and diagnosis of the presence or absence of

XX CC optineurin-associated glaucoma or of an optineurin-associated increased

XX CC risk of glaucoma are described, in which a sample is tested for the

XX CC presence of these gene sequence alterations or for alterations in the

XX CC expression or activity of the optineurin protein. Also described are

XX CC methods of therapy of glaucoma, including gene therapy methods.

XX SQ Sequence 2008 BP; 656 A; 421 C; 549 G; 382 T; 0 U; 0 Other;

Query Match

92.8%; Score 1927.4; DB 12; Length 2008;



Best Local Similarity 96.6%; Pred. No. 0; Matches 2007; Conservative 0; Mismatches 1; Indels 69; Gaps 1;			
QY	1	ATCCCGGTGGGAGTTCTCTCCAGGCGGCACGATCCGAGGAAACAGTCAACCTGAGCGA	60
Db	1	ATCCCGGTGGGAGTTCTCTCCAGGCGGCACGATCCGAGGAAACAGTCAACCTGAGCGA	60
QY	61	AGCCAAAGCCGGCGGCGAGGTGTGGCTTTGATAGCTGGTGGTGCACCTTCCTGGCCTTGGA	120
Db	61	AGCCAAAGCCGGCGGCGAGGTGTGGCTTTGATAGCTGGTGGTGCACCTTCCTGGCCTTGGA	120
QY	121	TGAGCGTACGCTCTGTAAACCAATTCCTCACCCTTTGAAACAGCTGCTGGTTTCAGC	180
Db	121	TGAGCGTACGCTCTGTAAACCAATTCCTCACCCTTTGAAACAGCTGCTGGTTTCAGC	180
QY	181	ATTAATGAGATTAGTCAGTGAAGGCTGGTGTGCTGAGTCCGCACATA-----	230
Db	181	ATTAATGAGATTAGTCAGTGAAGGCTGGTGTGCTGAGTCCGCACATA-----	230
QY	241	AAATGTCCAAAATGTAACTGGAGAGAAAGTGGGCAACTTTTGGAGTGACTTTTCCACAGG	300
Db	231	-----G 231	
QY	301	AATCTGTCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAGAGGAGACAGCCCCAG	360
Db	232	AATCTGTCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAGAGGAGACAGCCCCAG	291
QY	361	TGAAACACAGGAAATGGACCCCTCCACCTGGCCCAACCAACCTGGACAGCTTTACCCC	420
Db	292	TGAAACACAGGAAATGGACCCCTCCACCTGGCCCAACCAACCTGGACAGCTTTACCCC	351
QY	421	GGAGGAGCTCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCAACAGCTGAAAGAGC	480
Db	352	GGAGGAGCTCTGCAGCAGATGAAGAGCTCTCTGACCGAGAACCAACAGCTGAAAGAGC	411
QY	481	CATGAAAGCTAAATAACAGCCATGAAGAGGAGATTGAGGAGCTTTGGSCCTGGACAGA	540
Db	412	CATGAAAGCTAAATAACAGCCATGAAGAGGAGATTGAGGAGCTTTGGSCCTGGACAGA	471
QY	541	GAACAGAGGAGAGACCCAGTTTGTGAGATACAGAGCAGAGACAGAGAGAGAGAGCTCT	600
Db	472	GAACAGAGGAGAGAGCCAGTTTGTGAGATACAGAGCAGAGAGAGAGAGAGAGCTCT	531
QY	601	AATGGCCTTGAGTCATGAGAAATGAGAAATGAAAGGAGAGCTTTGGAAAACTAAAGGGA	660
Db	532	AATGGCCTTGAGTCATGAGAAATGAGAAATGAAAGGAGAGCTTTGGAAAACTAAAGGGA	591
QY	661	ATCAGAAAGTCTCTGAGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGGGA	720
Db	592	ATCAGAAAGTCTCTGAGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGGGA	651
QY	721	GCAGGAAAGGACAGCTCAGGACCCAGGTGGTGGGCTACAGAGCAGAGAGAGAGACCT	780
Db	652	GCAGGAAAGGACAGCTCAGGACCCAGGTGGTGGGCTACAGAGCAGAGAGAGAGACCT	711
QY	781	GTGGGCTCTGCTGCTGAACTGAGCTCAAGCTGAACTCCAGGGCTCTCTCAGAGATTC	840
Db	712	GTGGGCTCTGCTGCTGAACTGAGCTCAAGCTGAACTCCAGGGCTCTCTCAGAGATTC	771
QY	841	CTTTGTTGAAATTAGGATGGCTGAAGAGAGAGAGAGAGGTTCAGTAAAGAAATCAAGCA	900
Db	772	CTTTGTTGAAATTAGGATGGCTGAAGAGAGAGAGAGAGGTTCAGTAAAGAAATCAAGCA	831
QY	901	TAGTCTGGGCCCAAGAGAGTCTCCACTGGCAGCGGCTTGTCTAAATATAGGAGCAG	960
Db	832	TAGTCTGGGCCCAAGAGAGTCTCCACTGGCAGCGGCTTGTCTAAATATAGGAGCAG	891
QY	961	ATCTGAGATGGGGCCAAAGATTAATTCGAAACATGAGGAGTTAACTGTGAGCCAGCTCT	1020
Db	892	ATCTGAGATGGGGCCAAAGATTAATTCGAAACATGAGGAGTTAACTGTGAGCCAGCTCT	951
QY	1021	GCTGTGCTTAAGGAGAGGAAATCAGAAAGTGGAGAGACTTGAAGTTGCATCTCAAGGAGC	1080

Db	952	GCTGTGCTTAAGGAGGAAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGAGGC	1011
QY	1081	CAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCTTCTGAGATTGAACCCCA	1140
Db	1012	CAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCTTCTGAGATTGAACCCCA	1071
QY	1141	GCACAGGGGAGCACAGAGAAAGAGATGATCAAGAGAAAGCCCGGAGACTGTTGGAAG	1200
Db	1072	GCACAGGGGAGCACAGAGAAAGAGATGATCAAGAGAAAGCCCGGAGACTGTTGGAAG	1131
QY	1201	CGAAGTGAAGCACCTCAAGTGCATCTCTGTTTAAAGGAGCTTCAAGAGAGCTCA	1260
Db	1132	CGAAGTGAAGCACCTCAAGTGCATCTCTGTTTAAAGGAGCTTCAAGAGAGCTCA	1191
QY	1261	TACAAAACTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAAGTGTGAGGCCCT	1320
Db	1192	TACAAAACTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAAGTGTGAGGCCCT	1251
QY	1321	TGAAAGGAAAAATTCGCAATTCATCAGAGTTGAATGAAAGCAAGAGACTTGTATTATAC	1380
Db	1252	TGAAAGGAAAAATTCGCAATTCATCAGAGTTGAATGAAAGCAAGAGACTTGTATTATAC	1311
QY	1381	TACAAAAAGTTAGAGCTACAAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGC	1440
Db	1312	TACAAAAAGTTAGAGCTACAAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGC	1371
QY	1441	TAAAAACAGAGGATGAAAAAGTCCAAATTTAACTGTGTCTACAGATGACACACAAAGCTTCT	1500
Db	1372	TAAAAACAGAGGATGAAAAAGTCCAAATTTAACTGTGTCTACAGATGACACACAAAGCTTCT	1431
QY	1501	TCAGAAACATAATATATGCAATTTGAAAAAATTTGAGGAACTAACAGAAAAAGTTCAGAAAA	1560
Db	1432	TCAGAAACATAATATATGCAATTTGAAAAAATTTGAGGAACTAACAGAAAAAGTTCAGAAAA	1491
QY	1561	AGTGGACAGGGCAGTGTGAAAGAACTGAGTGAAGAACTGGAACCTGGAGAGAGAGCTCT	1620
Db	1492	AGTGGACAGGGCAGTGTGAAAGAACTGAGTGAAGAACTGGAACCTGGAGAGAGAGCTCT	1551
QY	1621	GGCTTCCAAACAGCTGCAAAATGAGTGAATGAAGCAAAACCAATTTGCCAAGCAGGAGGA	1680
Db	1552	GGCTTCCAAACAGCTGCAAAATGAGTGAATGAAGCAAAACCAATTTGCCAAGCAGGAGGA	1611
QY	1681	CCTGGAACCATGACCATCTCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGC	1740
Db	1612	CCTGGAACCATGACCATCTCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGC	1671
QY	1741	TGAAAGAGCAGCAGAGAGAAAAATTCATCAGGAAAAAGGAGCAACTGGCATTGCAGCTGGC	1800
Db	1672	TGAAAGAGCAGCAGAGAGAAAAATTCATCAGGAAAAAGGAGCAACTGGCATTGCAGCTGGC	1731
QY	1801	AGTTCTGCTGAAAGAGATGATGCTTTTGAAGACGAGGAGCAGGCTCTTGTGATGAGAT	1860
Db	1732	AGTTCTGCTGAAAGAGATGATGCTTTTGAAGACGAGGAGCAGGCTCTTGTGATGAGAT	1791
QY	1861	GCAGAGTCTGATGAGGCGAGAAACAAAGTGACTTGAACAGAGGCTTACCTGTTCAAAG	1920
Db	1792	GCAGAGTCTGATGAGGCGAGAAACAAAGTGACTTGAACAGAGGCTTACCTGTTCAAAG	1851
QY	1921	AGGAGCTGAGGACAGGAGCTGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA	1980
Db	1852	AGGAGCTGAGGACAGGAGCTGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA	1911
QY	1981	GTGTGAGAGAGTTTCTCCCTGACATAGACAGCTTTACAGATTCACGTGATGATTCATCAT	2040
Db	1912	GTGTGAGAGAGTTTCTCCCTGACATAGACAGCTTTACAGATTCACGTGATGATTCATCAT	2000
QY	2041	TTAAGTGTGATGATTCACCTCCCAAACTGTTGGT	2077
Db	1972	TTAAGTGTGATGATTCACCTCCCAAACTGTTGGT	2008

ID AC03997 standard; cDNA; 1856 BP.  
XX AC ACF03997;  
XX 23-SEP-2003 (first entry)  
DT Human optineurin isoform 2 encoding cDNA SEQ ID NO:3.  
DE Human; optineurin; OPTN; chromosome 10; 10p14; glaucoma; ophthalmic;  
KW gene therapy; gene; ss.  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 90..1823  
FT /\*tag= a  
FT /product= "optineurin isoform 2"  
PN W02003056037-A1.  
XX  
XX 10-JUL-2003.  
XX 18-DEC-2002; 2002WO-US041116.  
XX  
XX 24-DEC-2001; 2001US-0344754P.  
PR 30-JAN-2002; 2002US-00060981.  
PR 28-FEB-2002; 2002US-00090118.  
PR 25-OCT-2002; 2002US-00281454.  
XX  
XX (UYCO-) UNIV CONNECTICUT.  
PA (SGEO-) ST GEORGES ENTERPRISES LTD.  
XX  
XX Sarfarazi M, Rezaie T, Child AH;  
XX WPI: 2003-598273/56.  
DR P-PSDB; ABR82078.  
XX  
XX Diagnosing the presence or absence of optineurin-associated glaucoma or  
PT optineurin-associated increased risk of glaucoma in an individual by  
PT assessing a test sample for the presence or absence of an alteration in  
PT the optineurin gene.  
XX  
XX Claim 1; Page 72-75; 83pp; English.  
XX  
XX The present invention describes a method (M1) for diagnosing the presence  
CC or absence of optineurin-associated glaucoma or an optineurin-associated  
CC increased risk of glaucoma in an individual comprising detecting the  
CC presence or absence of an alteration in expression, composition or  
CC activity of an optineurin nucleic acid or polypeptide, which is  
CC indicative of the presence or absence, respectively, of the optineurin-  
CC associated glaucoma. Optineurin has ophthalmic activity and can be used  
CC in gene therapy. Optineurin therapeutic agents can be used for the  
CC manufacture of a medicament for the treatment of glaucoma or of an  
CC increased risk for glaucoma. Human optineurin is located on chromosome  
CC 10, more specifically to 10p14. The present sequence encodes human  
CC optineurin isoform 2, which is used in the exemplification of the present  
CC invention  
XX  
SQ Sequence 1856 BP; 625 A; 382 C; 509 G; 340 T; 0 U; 0 Other;  
  
Query Match 85.7%; Score 1779.4; DB 9; Length 1856;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1780; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 297 CAGGAATTCGCAATGCCATCAACCTCTCAGCTGCCTCCTGAAAGGAGGACGACC 356  
DB 76 CAGGAATTCGCAATGCCATCAACCTCTCAGCTGCCTCCTGAAAGGAGGACGACC 135  
QY 357 CCAGTGAAGCAGAGGAAATGGACCCGCCACCTGGCCACCCAAACCTGGACACGTTTA 416  
DB 136 CCAGTGAAGCAGAGGAAATGGACCCGCCACCTGGCCACCCAAACCTGGACACGTTTA 195  
QY 417 CCCCGGAGGAGCTGCTGTCAGCAGATGAAGAGCTCCTGACCAAGAACCCACGCTGAAG 476

196 CCCCGGAGGAGCTGCTGTCAGCAGATGAAGAGCTCCTGACCGAGAACCCACGAGTGAAG 255  
QY 477 AAGCCATGAAGCTTAATTAATCAAGCCATGAAGGAGATTTGAGGAGCTTTGGCGCTGGA 536  
DB 256 AAGCCATGAAGCTTAATTAATCAAGCCATGAAGGAGATTTGAGGAGCTTTGGCGCTGGA 315  
QY 537 CAGAGAAACAGAGAGGAAAGCCAGCTTTTGTAGATACAGAGCAAGAGCAAAAGAGC 596  
DB 316 CAGAGAAACAGAGAGGAAAGCCAGCTTTTGTAGATACAGAGCAAGAGCAAAAGAGC 375  
QY 597 GTCTAATGGCTTGGTATGATGAGAAATGAAGAGAGAGCTTTGGAAAACTAAAG 656  
DB 376 GTCTAATGGCTTGGTATGATGAGAAATGAAGAGAGAGCTTTGGAAAACTAAAG 435  
QY 657 GGAATACAGAAAGCTCATCTGAGACCCCACTGATGACTCCAGCTTCCCGAGGCGGAG 716  
DB 436 GGAATACAGAAAGCTCATCTGAGACCCCACTGATGACTCCAGCTTCCCGAGGCGGAG 495  
QY 717 CGGAGCAGGAAAGGACACAGCTCAGGACCCAGGCTGAGGCTACAAGCAGAGAGGCGAG 776  
DB 496 CGGAGCAGGAAAGGACACAGCTCAGGACCCAGGCTGAGGCTACAAGCAGAGAGGCGAG 555  
QY 777 ACCTTTGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG 836  
DB 556 ACCTTTGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG 615  
QY 837 ATTCTTTTGTGAATTAGGATGGCTGAAGGAGAGCAGAGGCTGAGTAAAGAAATCA 896  
DB 616 ATTCTTTTGTGAATTAGGATGGCTGAAGGAGAGCAGAGGCTGAGTAAAGAAATCA 675  
QY 897 AGCATAGTCTCGGCGCCACAGAAACAGCTCTCACTGGCACGGCATTCCTAAATATAGGA 956  
DB 676 AGCATAGTCTCGGCGCCACAGAAACAGCTCTCACTGGCACGGCATTCCTAAATATAGGA 735  
QY 957 GCAGATCTGAGATGGGCGCAAGAAATTAATTCGAACATGAGGAGTAACTGTGAGCCAGC 1016  
DB 736 GCAGATCTGAGATGGGCGCAAGAAATTAATTCGAACATGAGGAGTAACTGTGAGCCAGC 795  
QY 1017 TCCTGCTGCTTAAGGAGGAGGAAATCAGAGGTGGAGAGACTTGAAGTTCACCTCAAGG 1076  
DB 796 TCCTGCTGCTTAAGGAGGAGGAAATCAGAGGTGGAGAGACTTGAAGTTCACCTCAAGG 855  
QY 1077 AGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAGTAATCGTTCTGAGATTGAAA 1136  
DB 856 AGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAGTAATCGTTCTGAGATTGAAA 915  
QY 1137 CCAGACAGAGGAGGAGCAGAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTG 1196  
DB 916 CCAGACAGAGGAGGAGCAGAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTG 975  
QY 1197 GAAGCGAAGTGGAGGAGCAGTGAACCTCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG 1256  
DB 976 GAAGCGAAGTGGAGGAGCAGTGAACCTCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG 1035  
QY 1257 CTCATCAAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGTCAAGG 1316  
DB 1036 CTCATCAAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGTCAAGG 1095  
QY 1317 CCCTTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAAAGAGAGCTGTTT 1376  
DB 1096 CCCTTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAAAGAGAGCTGTTT 1155  
QY 1377 ATACTAAACAAAAGTTAGAGCTTCAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAC 1436  
DB 1156 ATACTAAACAAAAGTTAGAGCTTCAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAC 1215  
QY 1437 AGGCTAAACAGAGGATGAAGTCCAAATTAATCTGCTACAGATGACACAAAGC 1496  
DB 1216 AGGCTAAACAGAGGATGAAGTCCAAATTAATCTGCTACAGATGACACAAAGC 1275  
QY 1497 TTCTTCAAGAACATAATAATGCAATTGAAAAACAATTGAGGAACCTTAAACAGAAAAAGAGTCAG 1556

Db 1276 TTCTTCAAGAACATAATAATGCAATTGAAACAATTCAGGAACTAACAGAAAAGAGTCAG 1335  
QY 1557 AAAAAAGTGGACAGGGCAGTGTGAAGGAACTGAGTGAAAAAATCTGGAACTGGCAGAGAAAG 1616  
Db 1336 AAAAAAGTGGACAGGGCAGTGTGAAGGAACTGAGTGAAAAAATCTGGAACTGGCAGAGAAAG 1395  
QY 1617 CTCTGGCTTCCAAACAGCTGCAAAATGGAATGAATGAAGCAAAACCAATGCAAGCAGGAAG 1676  
Db 1396 CTCTGGCTTCCAAACAGCTGCAAAATGGAATGAATGAAGCAAAACCAATGCAAGCAGGAAG 1455  
QY 1677 AGCACTGGAAACCATGACCTCCTCAGGGCTCAGATGGAAGTTTACTGTTCTCTGATTTTC 1736  
Db 1456 AGCACTGGAAACCATGACCTCCTCAGGGCTCAGATGGAAGTTTACTGTTCTCTGATTTTC 1515  
QY 1737 ATGCTGAAAGAGCAGCGAGAGAGAAAAATTCATGAGGAAAGGACAACTGGCAATTCGAGC 1796  
Db 1516 ATGCTGAAAGAGCAGCGAGAGAGAAAAATTCATGAGGAAAGGACAACTGGCAATTCGAGC 1575  
QY 1797 TGGCAGTTCTGTGAAGAGAAATGATGCTTTTGAAGCAGGAGGAGCGAGCTCTTGATGG 1856  
Db 1576 TGGCAGTTCTGTGAAGAGAAATGATGCTTTTGAAGCAGGAGGAGCGAGCTCTTGATGG 1635  
QY 1857 AGATGAGAGTCTGATGGGCGAGAACAGTCACTGACAGCAGGCTTACTTGTTC 1916  
Db 1636 AGATGAGAGTCTGATGGGCGAGAACAGTCACTGACAGCAGGCTTACTTGTTC 1695  
QY 1917 AAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCATTCCTGCC 1976  
Db 1696 AAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCATTCCTGCC 1755  
QY 1977 CCAAGTGTGAGAGGTTCTGCTGACATAGACACGTTACAGATTCACGTTGATGGATGCA 2036  
Db 1756 CCAAGTGTGAGAGGTTCTGCTGACATAGACACGTTACAGATTCACGTTGATGGATGCA 1815  
QY 2037 TCATTTAAGTGTGATGATATCACCTCCCAAAACTGTGGT 2077  
Db 1816 TCATTTAAGTGTGATGATATCACCTCCCAAAACTGTGGT 1856

RESULT 13  
ADO43185  
ID ADO43185 standard; cDNA; 1856 BP.  
XX ADO43185;  
AC  
XX  
XX  
DT 29-JUL-2004 (first entry)  
XX  
DE Human optineurin isoform 2 cDNA, associated with glaucoma.  
XX  
XX Human; optineurin; glaucoma; diagnosis; gene therapy; ophthalmological;  
KW gene; chromosome 10p14; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key Location/Qualifiers  
FT CDS 90..1823  
FT /\*tag= a  
FT /product= "Human optineurin isoform 1"  
XX  
XX WO2004039312-A2.  
XX  
XX 13-MAY-2004.  
XX  
XX 26-JUN-2003; 2003WO-US020165.  
XX  
XX 25-OCT-2002; 2002US-00281457.  
XX  
XX (UYCO-) UNIV CONNECTICUT.  
PA (SGEO-) ST GEORGES ENTERPRISES LTD.  
XX  
XX Sarfarazi M, Rezaie T, Child AH;  
XX  
XX WPI; 2004-376046/35.  
DR

DR P-PSDB; ADO43186.  
DR GENBANK; AF420372.  
XX  
XX New optineurin nucleic acids and polypeptides having sequence  
PT alterations, which indicates the presence of an optineurin-associated  
PT (risk of) glaucoma, useful for detecting or diagnosing glaucoma, e.g.  
PT primary open angle glaucoma.  
XX  
PS Claim 1; SEQ ID NO 3; 110pp; English.  
XX  
XX The present sequence is that of cDNA encoding isoform 2 of human  
CC optineurin (optic neuropathy inducing protein). Mutation of the  
CC optineurin gene on chromosome 10 is associated with primary open angle  
CC glaucoma. In specific embodiments of the invention, the alteration is  
CC (numbering according to optineurin isoform 1 cDNA ADO43183): a change  
CC from GAG to AAG at codon 50 of the optineurin gene; an insertion of AG  
CC after codon 127; a change from CGG to CAG at codon 545; or a combination  
CC of one or more of these. These alterations are associated with glaucoma,  
CC and the presence of one or more of these alterations is diagnostic for  
CC glaucoma. In another embodiment, the alteration is a change from ATG to  
CC AAG at codon 98. The presence of this alteration is indicative of an  
CC increased risk of glaucoma, and is diagnostic of this increased risk.  
CC Other alterations include a change from CCC to GCC at codon 16, a change  
CC from CAG to CAC at codon 42, a change from GAA to GTA at codon 92, and a  
CC change from GAA to AAA at codon 322. Alterations include combinations of  
CC alterations such as combinations of alterations associated with glaucoma  
CC and those associated with an increased risk of glaucoma. Methods of  
CC detection, prognosis and diagnosis of the presence or absence of  
CC optineurin-associated glaucoma or of an optineurin-associated increased  
CC risk of glaucoma are described, in which a sample is tested for the  
CC presence of these gene sequence alterations or for alterations in the  
CC expression or activity of the optineurin protein. Also described are  
CC methods of therapy of glaucoma, including gene therapy methods.  
XX  
SQ Sequence 1856 BP; 625 A; 382 C; 509 G; 340 T; 0 U; 0 Other;  
Query Match 85.7%; Score 1779.4; DB 12; Length 1856;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1780; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 297 CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGAGCAGGCC 356  
Db 76 CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGAGCAGGCC 135  
QY 357 CCAGTGAAAGCAGAGAAATGGACCCGCCCACTGGCCCAACCCAAACCTGGACACGTTTA 416  
Db 136 CCAGTGAAAGCAGAGAAATGGACCCGCCCACTGGCCCAACCCAAACCTGGACACGTTTA 195  
QY 417 CCCCAGGAGGCTGTGTCAGCAGATGAAGAGCTCTGACCAAGAACCCAGCAGCCAGCTGAAAG 476  
Db 196 CCCCAGGAGGCTGTGTCAGCAGATGAAGAGCTCTGACCCGAGAACCCAGCAGCTGAAAG 255  
QY 477 AAGCCATGAAGCTTAAATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTCGGCCCTGGA 536  
Db 256 AAGCCATGAAGCTTAAATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTCGGCCCTGGA 315  
QY 537 CAGAGAAACAGAGGAGAAACGCCAGCTTTTGTGATACAGACCAAGAAAGCAAAAGAGC 596  
Db 316 CAGAGAAACAGAGGAGAAACGCCAGCTTTTGTGATACAGACCAAGAAAGCAAAAGAGC 375  
QY 597 GTCTAATGGCCTTGAGTCATGGAATGAGAAATGAGGAGAGCTTGGAAACTAAAG 656  
Db 376 GTCTAATGGCCTTGAGTCATGGAATGAGAAATGAGGAGAGCTTGGAAACTAAAG 435  
QY 657 GGAAATCAGAAAGGTCTATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG 716  
Db 436 GGAAATCAGAAAGGTCTATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG 495  
QY 717 CGGAGCAGGAAAAAGGACAGCTCAGACCCAGGTGTGAGGCTTACAGCAGAGAGAGCAG 776  
Db 496 CGGAGCAGGAAAAAGGACAGCTCAGACCCAGGTGTGAGGCTTACAGCAGAGAGAGCAG 555  
QY 777 ACCTGTTGGGCATCGTGTCTGAACTCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG 836

Db 556 ACCTGTTGGGCATCGTGTGAACGTCAGCTCAAGCTGAACTCCAGGGCTCCTCAGAAG 615  
QY 837 ATTCCTTTGTTGAAATAGGATGCTGAAGGAGAGCAGAGGCTCAGTAAAGAAATCA 896  
Db 616 ATTCCTTTGTTGAAATAGGATGCTGAAGGAGAGCAGAGGCTCAGTAAAGAAATCA 675  
QY 897 AGCATAGTCTGGGCCCCACGAGAACAGTCTCCACTGCGACGGCAATCTCTAAATATAGGA 956  
Db 676 AGCATAGTCTGGGCCCCACGAGAACAGTCTCCACTGCGACGGCAATCTCTAAATATAGGA 735  
QY 957 GCAGATCTGCAGATGGGGCCCAAGAAATTAATCTCGAACATGAGGATTAATCTGTGAGCCAGC 1016  
Db 736 GCAGATCTGCAGATGGGGCCCAAGAAATTAATCTCGAACATGAGGATTAATCTGTGAGCCAGC 795  
QY 1017 TCCTGCTGTGCTTAAGCGAAGGGGAATCAGAAGGTGGAGAGACTTTGAAGTTTGCACCTCAAGG 1076  
Db 796 TCCTGCTGTGCTTAAGCGAAGGGGAATCAGAAGGTGGAGAGACTTTGAAGTTTGCACCTCAAGG 855  
QY 1077 AGGCCAAAGAAAGATTTTCAGATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAA 1136  
Db 856 AGGCCAAAGAAAGATTTTCAGATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAA 915  
QY 1137 CCCAGACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAAAGGCCCGGAGACTGTTG 1196  
Db 916 CCCAGACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAAAGGCCCGGAGACTGTTG 975  
QY 1197 GAAGCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGACTTCAAGAGG 1256  
Db 976 GAAGCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGACTTCAAGAGG 1035  
QY 1257 CTCATACAAAACCTCAGCGAAGCTGAGCTAATGAAGAAAGAGACTTCAAGAAAAGTGTGAGG 1316  
Db 1036 CTCATACAAAACCTCAGCGAAGCTGAGCTAATGAAGAAAGAGACTTCAAGAAAAGTGTGAGG 1095  
QY 1317 CCCTTGAAGGAAAAATCTGCAATTCATCAGAGTTGAATGAAGAAAGAGAGCTGTTT 1376  
Db 1096 CCCTTGAAGGAAAAATCTGCAATTCATCAGAGTTGAATGAAGAAAGAGAGCTGTTT 1155  
QY 1377 ATACTTAACAAAAAGTTAGAGCTCAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAC 1436  
Db 1156 ATACTTAACAAAAAGTTAGAGCTCAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAC 1215  
QY 1437 AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACAAACAGC 1496  
Db 1216 AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACACAGC 1275  
QY 1497 TTCTTCAAGAACATATATGCAATTTGAAAACAAATTTGAGGAACTAAACAAGAAAAGAGTCAAG 1556  
Db 1276 TTCTTCAAGAACATATATGCAATTTGAAAACAAATTTGAGGAACTAAACAAGAAAAGAGTCAAG 1335  
QY 1557 AAAAAAGTGGACGGGAGTCTGAAGGAACCTGAGTGAAGAACTGGAACCTGGACGAGAGAGG 1616  
Db 1336 AAAAAAGTGGACGGGAGTCTGAAGGAACCTGAGTGAAGAACTGGAACCTGGACGAGAGAGG 1395  
QY 1617 CTCTGGCTTCCAAACAGCTCAAAATGATGAATGAAGCAAAACCAATTCGCAACGAGCAAG 1676  
Db 1396 CTCTGGCTTCCAAACAGCTCAAAATGATGAATGAAGCAAAACCAATTCGCAACGAGCAAG 1455  
QY 1677 AGACCTGGAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTC 1736  
Db 1456 AGACCTGGAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTC 1515  
QY 1737 ATGCTGAAGAGCAGCGAGAGAGAAATTCATCAGGAAAGAGGAGCACTGGCAATTCGAGC 1796  
Db 1516 ATGCTGAAGAGCAGCGAGAGAGAAATTCATCAGGAAAGAGGAGCACTGGCAATTCGAGC 1575  
QY 1797 TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGAGGAGGAGCTGCTTCTGATGG 1856  
Db 1576 TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGAGGAGGAGCTGCTTCTGATGG 1635  
QY 1857 AGATGAGAGTCTCTATGGGGCGAGAACAAAGTCACTCTGACCGAGCGGCTTACCTTGTTC 1916

Db 1636 AGATGCAGAGTCGTCTATGGGGCGAGAACAAAGTGACTCTGACCAGAGGCTTACCTTGTTC 1695  
QY 1917 AAAGAGAGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCC 1976  
Db 1696 AAAGAGAGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCC 1755  
QY 1977 CCAAGTGTGAGAGGTTCTGCTCTGACATACACAGCTTACAGATTCAGTGTGATGATGCA 2036  
Db 1756 CCAAGTGTGAGAGGTTCTGCTCTGACATACACAGCTTACAGATTCAGTGTGATGATGCA 1815  
QY 2037 TCATTTAAGTGTGATGATGATACCTCCCAAAACTGTTGTT 2077  
Db 1816 TCATTTAAGTGTGATGATGATACCTCCCAAAACTGTTGTT 1856

RESULT 14  
ADRI4212  
ID ADRI4212 standard; DNA; 2327 BP.  
XX  
AC ADRI4212;  
XX  
XX 21-OCT-2004 (first entry)  
XX  
XX Human NF-kappaB pathway-associated gene SeqID213.  
DE  
XX  
XX NF-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide;  
KW antiarthritis; antirheumatic; gastrointestinal-Gen; antiasthmatic;  
KW antiarteriosclerotic; immunomodulator; cerebroprotective; vasotropic;  
KW immunosuppressive; vulnery; gene therapy; immune disorder;  
KW inflammatory disorder; NF-kappaB regulation; cancer; aberrant apoptosis;  
KW hepatic disorder; Hodgkin's lymphoma; haematopoietic tumour;  
KW hyper-IGM syndrome; hypohidrotic ectodermal dysplasia;  
KW X-linked anhidrotic ectodermal dysplasia; immunodeficiency;  
KW viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza;  
KW rheumatoid arthritis; host cell survival; evasion of immune response;  
KW atherosclerosis; cachexia; inflammatory bowel disease; colitis; asthma;  
KW autoimmune disorder; hyper immune activity;  
KW aberrant acute phase response; hypercongenital condition; birth defect;  
KW necrotic lesion; wound; organ transplant rejection;  
KW aberrant signal transduction; proliferating disorder; cancer;  
KW HIV propagation; gene; ds; human.  
XX  
OS Homo sapiens.  
XX  
XX WO2004065577-A2.  
XX  
XX 05-AUG-2004.  
XX  
XX 13-JAN-2004; 2004WO-US000798.  
XX  
XX 14-JAN-2003; 2003US-0440068P.  
XX 12-MAY-2003; 2003US-0469757P.  
XX  
XX (BRIM ) BRISTOL-MYERS SQUIBB CO.  
XX  
XX Nadler SG, Neubauer MG, Feder JN, Carman J;  
XX  
XX WPI; 2004-562168/54.  
XX P-PSDB; ADRI4213.  
XX  
XX New isolated polynucleotides and polypeptides associated with NF-kappaB  
XX pathway, useful for diagnosing, treating, or preventing disorders or  
XX diseases associated with NF-kappaB pathway.  
XX  
XX Claim 1; SEQ ID NO 213; 237pp; English.  
XX  
XX This invention relates to the novel association of protein sequences (and  
XX the genes which encode them) to the NF-kappaB pathway. The invention may  
XX be useful for the production of compounds with an antiinflammatory,  
XX cytostatic, hepatotropic, virucide, antiarthritis, antirheumatic,  
XX gastrointestinal-Gen, antiasthmatic, antiarteriosclerotic,  
XX immunomodulator, cerebroprotective, vasotropic, immunosuppressive or

CC vulnery activity or for gene therapy. The proteins and nucleotides are  
CC useful for diagnosing, preventing, treating, or ameliorating conditions  
CC or diseases associated with the NF-kappaB pathway. The condition is an  
CC immune disorder, an inflammatory disorder, an inflammatory disorder  
CC related to aberrant NF-kappaB regulation, cancer, aberrant apoptosis,  
CC hepatic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM  
CC syndromes, hypohidrotic ectodermal dysplasia, X-linked anhidrotic  
CC ectodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1,  
CC hepatitis B, hepatitis C, EBV, influenza, viral replication, host cell  
CC survival, evasion of immune responses, rheumatoid arthritis, inflammatory  
CC bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick  
CC syndrome, stroke, BAE, autoimmune disorders, disorders related to hyper  
CC immune activity, disorders related to aberrant acute phase responses,  
CC hypergenital conditions, birth defects, necrotic lesions, wounds,  
CC organ transplant rejection, conditions related to organ transplant  
CC rejection, disorders related to aberrant signal transduction,  
CC proliferating disorders, cancers and HIV propagation in cells infected  
CC with other viruses. The present sequence is that of a human gene which is  
CC subject to the novel association with the NF-kappaB pathway of the  
CC invention. Note: This sequence does not appear in the specification but  
CC was obtained by the indexer from Genbank.  
XX  
SQ Sequence 2327 BP; 747 A; 499 C; 636 G; 445 T; 0 U; 0 Other;

Query Match 85.7%; Score 1779.4; DB 13; Length 2327;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1780; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 297 CAGGAATCTGCAATGTCCTCACTCAACCTCTAGCTGCTCTACTGAAAGGGAGCAGCC 356  
DB 141 CAGGAATCTGCAATGTCCTCACTCAACCTCTAGCTGCTCTACTGAAAGGGAGCAGCC 200

QY 357 CCAGTGAAGCAGAGGAATGGACCCGCCCTGCGCCACCCACCAACCTGGACCAAGCCTGGAACCTTTA 416  
DB 201 CCAGTGAAGCAGAGGAATGGACCCGCCCTGCGCCACCCACCAACCTGGACCAAGCCTTTA 260

QY 417 CCCCGAGGAGCTGCTGCAGCAGATGAAGAGGCTCTGACCAAGAACCCACCGACTGAAAG 476  
DB 261 CCCCGAGGAGCTGCTGCAGCAGATGAAGAGGCTCTGACCAAGAACCCACCGACTGAAAG 320

QY 477 AAGCCATGAGCTTAATATACAGCCATGAAGGGAGATTTGAGGAGCTTTCGGCTTGA 536  
DB 321 AAGCCATGAGCTTAATATACAGCCATGAAGGGAGATTTGAGGAGCTTTCGGCTTGA 380

QY 537 CAGAGAAACAGAGGAGAAAGCGCAGTTTTTTTGAGATACAGAGCAAGCAAGCAAAAGAGC 596  
DB 381 CAGAGAAACAGAGGAGAAAGCGCAGTTTTTTTGAGATACAGAGCAAGCAAGCAAAAGAGC 440

QY 597 GTCTAATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAAGAGCTTGGAAACTAAAG 656  
DB 441 GTCTAATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAAGAGCTTGGAAACTAAAG 500

QY 657 GGAATACAGAAAGGTCTATCAGGACCCCACTGATGACTCCAGGCTTCCAGGCGCGAAG 716  
DB 501 GGAATACAGAAAGGTCTATCAGGACCCCACTGATGACTCCAGGCTTCCAGGCGCGAAG 560

QY 717 CGAGCAGGAAAGGACAGCTCAGGACCCAGGTGGTGGGCTACAGCAGAGAGGCGAG 776  
DB 561 CGAGCAGGAAAGGACAGCTCAGGACCCAGGTGGTGGGCTACAGCAGAGAGGCGAG 620

QY 777 ACCTGTTGGCATCGTGTCTGAACTGCAGTCAAGCTGAACTCCAGCGGCTCTCAGAAG 836  
DB 621 ACCTGTTGGCATCGTGTCTGAACTGCAGTCAAGCTGAACTCCAGCGGCTCTCAGAAG 680

QY 837 ATTCTTTGTTGAAATTTAGGATGGCTCAAGGAGAGCAGAGGCTCAGTAAAGAAATCA 896  
DB 681 ATTCTTTGTTGAAATTTAGGATGGCTCAAGGAGAGCAGAGGCTCAGTAAAGAAATCA 740

QY 897 AGCATAGCTCTGGGCCCAACAGAACAGCTCTCCATGCGCAGGCACTTCTCTAAATATAGGA 956  
DB 741 AGCATAGCTCTGGGCCCAACAGAACAGCTCTCCATGCGCAGGCACTTCTCTAAATATAGGA 800

QY 957 GCAGATCTGCAGATGGGGCCCAAGAAATTAATCTTCGAACATGAGGAGTTAACTGTGAGCCAGC 1016

DB 801 GCAGATCTGCAGATGGGGCCCAAGAAATTAATCTTCGAACATGAGGAGTTAACTGTGAGCCAGC 860

QY 1017 TCCTCTCTGCTGCCTAAGGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACCTCAAGG 1076

DB 861 TCCTCTCTGCTGCCTAAGGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACCTCAAGG 920

QY 1077 AGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAA 1136

DB 921 AGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAA 980

QY 1137 CCCGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGAAAGCCCGGAGAGACTGTTG 1196

DB 981 CCCGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGAAAGCCCGGAGAGACTGTTG 1040

QY 1197 GAAGCGAAGTGAAGCAGCTGAACCTCCAGGTGCACATCTCTGTTTAAAGAGACTTCAAGAGG 1256

DB 1041 GAAGCGAAGTGAAGCAGCTGAACCTCCAGGTGCACATCTCTGTTTAAAGAGACTTCAAGAGG 1100

QY 1257 CTCATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTCAAG 1316

DB 1101 CTCATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTCAAG 1160

QY 1317 CCCTTGAAGGAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTGTT 1376

DB 1161 CCCTTGAAGGAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTGTT 1220

QY 1377 ATACTAAACAAAAGTTAGAGCTTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAC 1436

DB 1221 ATACTAAACAAAAGTTAGAGCTTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAC 1280

QY 1437 AGGCTAAACACAGAGGATGAAAAGTCCAAATTAATCTGTGCTCAGATGACACACAAAGC 1496

DB 1281 AGGCTAAACACAGAGGATGAAAAGTCCAAATTAATCTGTGTACAGATGACACACAAAGC 1340

QY 1497 TTCTTCAGAAACATTAATATGATGATAAATGAGGAACTTAAACAGAAAGAGTCTAG 1556

DB 1341 TTCTTCAGAAACATTAATATGATGATAAATGAGGAACTTAAACAGAAAGAGTCTAG 1400

QY 1557 AAAAAAGTGACAGGGCAGTGTGAAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAAAG 1616

DB 1401 AAAAAAGTGACAGGGCAGTGTGAAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAAAG 1460

QY 1617 CTCTGCTTCCAAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAGGAAG 1676

DB 1461 CTCTGCTTCCAAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAGGAAG 1520

QY 1677 AGSACCTGAAACCACTGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTC 1736

DB 1521 AGSACCTGAAACCACTGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTC 1580

QY 1737 ATGCTGAAAGAGCAGCGAGAGAGAAATTCATGAGAAAGAGGCAACTGGCAATTCGAGC 1796

DB 1581 ATGCTGAAAGAGCAGCGAGAGAGAAATTCATGAGAAAGAGGCAACTGGCAATTCGAGC 1640

QY 1797 TGGCAGTTCTGCTGAAGAGATGATGCTTTTGAAGACGGAGCGCAGCTCTTGTATGG 1856

DB 1641 TGGCAGTTCTGCTGAAGAGATGATGCTTTTGAAGACGGAGCGCAGCTCTTGTATGG 1700

QY 1857 AGATGCAGAGTCTGATGGGGCGAGAAACAAAGTGAATTCGACAGAGGCTTACTTGTTC 1916

DB 1701 AGATGCAGAGTCTGATGGGGCGAGAAACAAAGTGAATTCGACAGAGGCTTACTTGTTC 1760

QY 1917 AAGAGGAGCTGAGGACAGGGAATGGCGGCAACAGCGGAATATTCGATTCATTCTCTGCC 1976

DB 1761 AAGAGGAGCTGAGGACAGGGAATGGCGGCAACAGCGGAATATTCGATTCATTCTCTGCC 1820

QY 1977 CCAAGTGTGGAGAGTTCTGCTGACATAGACAGTTACAGTTACAGTTACAGTTACAGTTAC 2036

DB 1821 CCAAGTGTGGAGAGTTCTGCTGACATAGACAGTTACAGTTACAGTTACAGTTACAGTTAC 1880

QY 2037 TCATTTTAAGTGTGATGATACCTCCCAAAAACTGTGTT 2077

Db 1881 TCATTAAAGTTGATGATACACCTCCCAAAACATGTTGGT 1921  
RESULT 15  
ADP23351  
XX ADP23351 standard; cDNA; 2327 BP.  
XX  
AC ADP23351;  
XX  
XX 18-NOV-2004 (first entry)  
XX  
XX PRO polypeptide encoding cDNA SEQ ID NO:445.  
XX  
XX ss; gene; PRO; antiinflammatory; antiarthritic; antirheumatic;  
KW immunosuppressive; osteopathic; antidiabetic; dermatological;  
KW antipsoriatic; antiallergic; antiasthmatic; hepatotropic; respiratory;  
KW gene therapy; immune system.  
XX  
XX Unidentified.  
XX  
XX WO2004041170-A2.  
XX  
XX 21-MAY-2004.  
XX  
XX 30-OCT-2003; 2003WO-US034312.  
XX  
XX 01-NOV-2002; 2002US-0423394P.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WT;  
PI Wu TD;  
XX  
XX WPI; 2004-419628/39.  
XX  
XX P-PSDB; ADP23352.  
XX  
XX New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematous, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
XX Claim 1; SEQ ID NO 445; 2940pp; English.  
XX  
XX The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematous, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, systemic  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polynuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polynuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence encodes a PRO protein of  
XX the invention.  
XX  
XX Sequence 2327 BP; 747 A; 499 C; 636 G; 445 T; 0 U; 0 Other;

	Query Match	85.7%	Score 1779.4;	DB 13;	Length 2327;
	Best Local Similarity	99.9%	Pred. No. 0;		
	Matches 1780;	Conservative	0;	Mismatches	1;
				Indels	0;
				Gaps	0;
Qy	297	CAGGAACCTTCTGCATATGTCATCAACCTCTCAGCTGCTCTCAGTGAAGAGGACAGCC	356		
Db	141	CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCTCTCAGTGAAGAGGACAGCC	200		
Qy	357	CCAGTGAAGACACAGGAATGGACCCCTCCACCTGGCCCAACCCCAACCTTGACACGTTTA	416		
Db	201	CCAGTGAAGACACAGGAATGGACCCCTCCACCTGGCCCAACCCCAACCTTGACACGTTTA	260		
Qy	417	CCCGGAGAGCTGCTGCAGCAGATGAAGAGCTCTTGACCAAGAACCCACAGCTGAAG	476		
Db	261	CCCGGAGAGCTGCTGCAGCAGATGAAGAGCTCTTGACCAAGAACCCACAGCTGAAG	320		
Qy	477	AAGCCATGAAGCTTAAATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTTGGCCTTGA	536		
Db	321	AAGCCATGAAGCTTAAATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTTGGCCTTGA	380		
Qy	537	CAGAGAAACAGAAAGGAAGACGCCAGTCTTTTGGAGATACAGACCAAGAACCAAGAGC	596		
Db	381	CAGAGAAACAGAAAGGAAGACGCCAGTCTTTTGGAGATACAGACCAAGAACCAAGAGC	440		
Qy	597	GTCTAATGGCTTTGAGTCATGAGAATGAGAAATTTGAAGGAAGAGCTTTGAAAACTAAAAG	656		
Db	441	GTCTAATGGCTTTGAGTCATGAGAATGAGAAATTTGAAGGAAGAGCTTTGAAAACTAAAAG	500		
Qy	657	GGAAATCAGAAAGGTCTGAGGACCCCACTGATGATCTCAGGCTTCCAGGGCCCAAG	716		
Db	501	GGAAATCAGAAAGGTCTGAGGACCCCACTGATGATCTCAGGCTTCCAGGGCCCAAG	560		
Qy	717	CGGAGCAGGAAAGGACAGCTCAGGACCCAGGTGGTGGCTACAGCAGAGAGAGCAG	776		
Db	561	CGGAGCAGGAAAGGACAGCTCAGGACCCAGGTGGTGGCTACAGCAGAGAGAGCAG	620		
Qy	777	ACCTGTGGCCTCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCTCTCAGAAG	836		
Db	621	ACCTGTGGCCTCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCTCTCAGAAG	680		
Qy	837	ATTCTCTTGTGTAATTAGGATCGCTGAGGAGACGAGAGGCTCAGTAAAAAGAAATCA	896		
Db	681	ATTCTCTTGTGTAATTAGGATCGCTGAGGAGACGAGAGGCTCAGTAAAAAGAAATCA	740		
Qy	897	AGCATAGTCTCTGGGCCACAGAGAACAGTCTCCACTGSCAGGCATTTGCTTAAATATAGGA	956		
Db	741	AGCATAGTCTCTGGGCCACAGAGAACAGTCTCCACTGSCAGGCATTTGCTTAAATATAGGA	800		
Qy	957	GCAGATCTGCAGATGGGGCCCAAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAGC	1016		
Db	801	GCAGATCTGCAGATGGGGCCCAAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAGC	860		
Qy	1017	TCCTGCTGTGCTTAAGGGAGGGAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGG	1076		
Db	861	TCCTGCTGTGCTTAAGGGAGGGAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGG	920		
Qy	1077	AGSCCAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTCTCGAGATTCGAA	1136		
Db	921	AGSCCAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTCTCGAGATTCGAA	980		
Qy	1137	CCGAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTGTTG	1196		
Db	981	CCGAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTGTTG	1040		
Qy	1197	GAAGCAAGTGGAGCACTGAACCTCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG	1256		
Db	1041	GAAGCAAGTGGAGCACTGAACCTCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG	1100		
Qy	1257	CTCATCAAAACCTCAGCGAAGCTGAGTAATGAAGAGAGACTTCAAGAAAGTGTGAGG	1316		
Db	1101	CTCATCAAAACCTCAGCGAAGCTGAGTAATGAAGAGAGACTTCAAGAAAGTGTGAGG	1160		
Qy	1317	CCCTTGAAGGAAAAATTTCTGCAATTTCCATCAGAGTTGAATGAAGAAAGAGAGCTTTGTTT	1376		





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QY 421 GGAGGAGCTGTCAGAGAGATGAAAGAGCTCTCTGACCAAGAAACACACAGCTGAAAGAAGC 480
Db 351 GGAGGAGCTGTCAGAGAGATGAAAGAGCTCTCTGACCGAGAAACACACAGCTGAAAGAAGC 410
QY 481 CATGAAGCTAAATTAATCAAGCCATGAAGAGGAGATTTGAGGAGCTTTGCGCCTGGACAGA 540
Db 411 CATGAAGCTAAATTAATCAAGCCATGAAGAGGCGTTTGGAGAGCTTTGCGCCTGGACAGA 470
QY 541 GAAACAGAAGGAAGAACCCAGTTTGTGATATCAGAGCAAAAGAAAGAGAGCGCTCT 600
Db 471 GAAACAGAAGGAAGAACCCAGTTTGTGATATCAGAGCAAAAGAAAGAGAGCGCTCT 530
QY 601 AATGSCCTTGATCATGAGATGAGAAATTTGAAGGAAAGAGCTTGGAAGAACTAAAGGGAA 660
Db 531 CATGSCCTTGATCATGAGATGAGAAATTTGAAGGAAAGAGCTTGGAAGAACTGAAAGGGAA 590
QY 661 ATCAGAAAGGTCACTCAGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGA 720
Db 591 ATCAGAAAGGTCACTCAGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGA 650
QY 721 GCAGGAAAAGGACCAAGCTCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAGGCGACCT 780
Db 651 GCAGGAAAAGGACCAAGCTCAGGACCCAGGTGACGAGGCTACAAGCAGAGAGGCGACCT 710
QY 781 GTTGGGCATCGTGTCTGAATGCGAGCTCAAGCTGAATCCAGCGGCTCTCTCAGAAGATTC 840
Db 711 GTTGGGCATCGTGTCTGAATGCGAGCTCAAACTGAATCCAGCGGCTCTCTCAGAAGATTC 770
QY 841 CTTTGTGTAATTAGGATGCTGAGAGAGAGAGAGAGAGAGGCTCAGTAAAGAAATCAAGCA 900
Db 771 CTTTGTGTAATTAGGATGCTGAGAGAGAGAGAGAGAGGTTTCAATAAAGAAATCAAGCA 830
QY 901 TAGTCTCTGGGCCCAAGAGACAGTCTCCACTGCGACGGCATTTGCTAAATATAGGAGCAG 960
Db 831 TAGTCTCTGGGCCCAAGAGACAGTCTCCATTTGGCAC-----GAGCAG 872
QY 961 ATCTGCAGATGGGGCCAAAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAGCTCT 1020
Db 873 ATCTGCAGAGGGGCCAAAGAAATTAATCTTGGAAACATGAGGAGTTAACTGTGAGCCAGCTCT 932
QY 1021 GCTGTGCTTAAGGGAAGGGAATCAGAAAGGTGGAGAGACTTGAAGTTGCACTCAAGGAGGC 1080
Db 933 GCTGTGCTTAAGGGAAGGGAATCAGAAAGGTGGAGAGACTTGAATTTGCACTCAAGGAGGC 992
QY 1081 CAAAGAAAGAGTTTCAGATTTGAAAGAGAAAAAAGTAACTGTTCTGAGATTGAAACCCCA 1140
Db 993 CAAAGAAAGAGTTTCAGATTTGAAAGAGAAAGCAAGTAACTGCTGAGATTGAAACCCCA 1052
QY 1141 GACAGAGGGGACGACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTGTGAAG 1200
Db 1053 GACAGAGGGGACGACAGAGAAAGAGAAACGAGGAAGAGAAAGGCCCGGAGACTGTGTGAAG 1112
QY 1201 CGAAGTGGAGACTGAACCTCAGGTGACATCTCTGTTTAAAGAGGTTCAAGAGGCTCA 1260
Db 1113 CGAAGTGGAGACTGAACCTCAGGTGACATCTCTGTTTAAAGAGGTTCAAGAGGCTCA 1172
QY 1261 TACAAACTCAGCGAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTGAGCCCT 1320
Db 1173 TACAAACTCAGTGAAGCCGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTGAGCCCT 1232
QY 1321 TGAAGGAAAAAATCTCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTATTATAC 1380
Db 1233 TGAAGGAAAAAATCTCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTATTATAC 1292
QY 1381 TAACAAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGC 1440
Db 1293 TAACAAAAAGTTAGAGCTACAAGTGGAAAGCATGCTCTCGGAAATCAAAATGGAACAGGC 1352
QY 1441 TAAACACAGAGATGAAGAGTCCAAATTAATCTGTGCTACAGATGACACACAAAGCTTCT 1500
Db 1353 TAAACACGAGGATGAAGAGTCCAAATTAATCTGTGCTACAGATGACACACAAAGCTTCT 1412
QY 1501 TCAAGACATAAATATGCAATTGAAACAAATTTAGGAACTAACAGAAAGAGTCAGAAAA 1560
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Db 1413 TCAGGAACATAATCATGTCATTGAAACAGATTGAGGAGCTAACAGAAAAAGAGTCAGAAAA 1472
QY 1561 AGTGGACAGGCGAGTCTGAGGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCT 1620
Db 1473 AGTGGACAGGCGAGTCTGAGGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCT 1532
QY 1621 GGCTTCCAAACAGCTGCAAAATGATGAAATGAAAGCAAAACCATTTGCCAAGCAGGAAGAGGA 1680
Db 1533 GGCTTCCAAACAGCTGCAAAATGATGAGATGAAGCAAACTATTGCCAAGCAGGAAGAGGA 1592
QY 1681 CCTGGAAAACATGACCATCTCTCAGGCTCAGAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGC 1740
Db 1593 CCTGGAAAACATGACCATCTCTCAGGCTCAGAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGC 1652
QY 1741 TGAAGAGCAGCAGAGAGAGAGAAATTCATGAGGAAAGAGGAGCAACTGGCATTTGCAGCTGGC 1800
Db 1653 TGAAGAGCAGCAGAGAGAGAGAAATTCATGAGGAAAGAGGAGCAACTGGCATTTGCAGCTGGC 1712
QY 1801 AGTTCTGCTGAAAGAGAAATGATGATCTTTCCGAAGACGGAGGAGGAGCTCTTGTATGGAGAT 1860
Db 1713 AGTTTCTGCTGAAAGAGAAATGATGCTTTTCGAAGATGGAGGAGGAGCTCTTGTATGGAGAT 1772
QY 1861 GCAGAGTCGTCTGAGGCGAGAAACAGTGAATCTGACACAGCAGGCTTACCTTGTTCAAAG 1920
Db 1773 GCAGAGTCGTCTGAGGCGAGAAACAGTGAATGACCCCGCAGCAGGCTTACCTTGTTCAAAG 1832
QY 1921 AGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCATTTCTGCCCCAA 1980
Db 1833 AGGAACTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCATTTCTGCCCCAA 1892
QY 1981 GTCTGAGAGGTTCTGCTGACATAGACAGCTTACAGATTACAGTGTGATGATGATCATCAT 2040
Db 1893 GTCTGAGAGGTTCTGCTGACATAGACAGCTTACAGATTACAGTGTGATGATGATCATCAT 1952
QY 2041 TTAAGTGTGATGATATCACCTCCCTCCCAAACTGTTGGT 2077
Db 1953 TTAGGTGTTGATGTGTACCTCCCTCCCAAACTGTTGGT 1989

RESULT 17
ADL14949
ID ADL14949 standard; DNA; 1734 BP.
XX
AC ADL14949;
XX
DT 06-MAY-2004 (first entry)
XX
Human glaucoma-related optineurin (OPTN) gene coding sequence.
XX
Human; glaucoma; optineurin; OPTN; diagnosis; gene; ds.
XX
Homo sapiens.
XX
Key Location/Qualifiers
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FT 167.369
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FT 370.552
FT /*tag= d
FT /number= 6
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FT /standard_name= "Single nucleotide polymorphism"
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FT exon 883. .998  
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FT exon 1243. .1401  
FT /*tag= m  
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FT exon 1533. .1612  
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FT /number= 15  
FT exon 1613. .1734  
FT /*tag= p  
FT /number= 16  
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XX EP1388590-A2.  
XX  
XX 11-FEB-2004.  
XX  
XX 29-JUL-2003; 2003EP-00447201.  
XX  
XX 02-AUG-2002; 2002JP-00226612.  
XX  
XX (SYSM-) SYSMEX CORP.  
XX  
XX Kouchi Y, Masago A, Takahata T;  
XX  
XX WPI; 2004-146134/15.  
XX  
XX Gene assay for predicting future onset of glaucoma, particularly primary  
XX open angle glaucoma or normal ocular tension glaucoma, comprises  
XX detecting a mutation of at least one base of the optineurin gene.  
XX  
XX Claim 2; SEQ ID NO 1; 3lpp; English.  
XX  
XX The present sequence is the coding sequence of the glaucoma-associated  
XX gene, OPTN (optineurin). The invention relates to a gene assay method for  
XX predicting future onset of primary open angle glaucoma and/or normal  
XX ocular tension glaucoma. This involves detecting a mutation in the OPTN  
XX gene coding sequence, specifically a substitution of G for A at position  
XX 619 and/or a substitution of A for G at position 898 of the present  
XX sequence. The mutation(s) is detected using a nucleic acid amplification  
XX method.  
XX  
XX Sequence 1734 BP; 599 A; 347 C; 471 G; 317 T; 0 U; 0 Other;  
XX  
XX Query Match 83.3%; Score 1730.8; DB 12; Length 1734;  
XX Best Local Similarity 99.9%; Pred. No. 0;  
XX Matches 1732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
XX 311 ATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGAGGACGCCCCAGTGAAAGCACA 370
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Db  
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371 GGAATATGGACCCCGCCACCTGGCCCGCCACCCAAACCTGGACACGTTTATCCCGGAGGAGCTG 430  
Db  
61 GGAATATGGACCCCGCCACCTGGCCCGCCACCCAAACCTGGACACGTTTATCCCGGAGGAGCTG 120  
QY  
431 CTGACGACGATGAAAAGAGCTCTGACCAAGAACCCACGCTGAAAGAACCCATGAAGCTA 490  
Db  
121 CTGACGACGATGAAAAGAGCTCTGACCGAGAACCCACGCTGAAAGAACCCATGAAGCTA 180  
QY  
491 AATAATCAAGCCATGAAAAGGAGATTGTAGGAGCTTTCCGCCCTGGACAGAGAAACAGAAG 550  
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611 AGTCATGAGATGAGAAATTTGAAGAGAGCTTTGAAAACCTAAAGGGGAAATCAGAAAGG 670  
Db  
301 AGTCATGAGATGAGAAATTTGAAGAGAGCTTTGAAAACCTAAAGGGGAAATCAGAAAGG 360  
QY  
671 TCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGCGGAGCAGGAAAAG 730  
Db  
361 TCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGCGGAGCAGGAAAAG 420  
QY  
731 GACCAAGCTCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAAAGCAGACCTGTTGGGCATC 790  
Db  
421 GACCAAGCTCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAAAGCAGACCTGTTGGGCATC 480  
QY  
791 GTGTCTGAACTGAGCTCAAGCTGAACTCCAGGGGCTCTCAGAGAAATTCCTTTGTGAA 850  
Db  
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851 ATTAGGATGGCTGAAGGAGAAAGCAGAGAGGTTCAGTAAAAAGAAATCAAGCATAGTCTCTGGG 910  
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911 CCCACGAGAACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGGAGCAGATCTGCAGAT 970  
Db  
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971 GGGGCCAAGAAATTAATCTCGAAATGAGGAGTTAACTGTGAGCCAGCTCCCTGCTGTCCTA 1030  
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1151 AGCAGAGAAAGAGAAATGATGAAGAAAGGCCCCCGGAGACTGTTGGAGCGGAAGTGGAA 1210  
Db  
841 AGCAGAGAAAGAGAAATGATGAAGAAAGGCCCCCGGAGACTGTTGGAGCGGAAGTGGAA 900  
QY  
1211 GCACCTCAACTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAACTC 1270  
Db  
901 GCACCTCAACTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAACTC 960  
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1271 AGCGAAGCTGAGCTAAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCCCTTTGAAAGGAAA 1330  
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QY  
1331 AATTCGCAATTCATCAGAGTTGAATGAAGCAGAGAGCTGTTTATATCTAACAAGAAAG 1390  
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1021 AATTCGCAATTCATCAGAGTTGAATGAAGCAGAGAGCTGTTTATATCTAACAAGAAAG 1080  
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Query Match	83.3%;	Score	1730.8;	DB	14;	Length	1734;		
Best Local Similarity	99.9%;	Pred. No.	0;						
Matches	1732;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	311	ATGTCCCATCAACTCTCAGCTGCTCTCAGCTGAAAGGAGGACGACGCCACGAGTGAAGGACA	370						
DB	1	ATGTCCCATCAACTCTCAGCTGCTCTCAGCTGAAAGGAGGACGACGCCACGAGTGAAGGACA	60						
QY	371	GGAAATGGACCCCCCACTTGGGCCACCCAAACCTTGGACAGCTTACCCCGGAGGAGCTG	430						
DB	61	GGAAATGGACCCCCCACTTGGGCCACCCAAACCTTGGACAGCTTACCCCGGAGGAGCTG	120						
QY	431	CTCGAGCAGATGAAGAGCTCTTGACCAAGAACCAACCAGCTGAAAGAGCATGAAGCTA	490						
DB	121	CTCGAGCAGATGAAGAGCTCTTGACCGAAGCAACCAAGCTGAAAGAGCATGAAGCTA	180						
QY	491	AATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTTTCGGCCCTGGACAGAGAAACAGAAG	550						
DB	181	AATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTTTCGGCCCTGGACAGAGAAACAGAAG	240						
QY	551	GAAGAACGCCAGTTTTTTTGAGATACAGAGCAAAAGAGCAAAAGAGCGTCTTAATGGCCCTTG	610						
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QY	611	AGTCATGAGAAATCAGAGAAATTTGAAGGAGAGCTTTGGAAACATAAAAGGGAAATCAGAAAGG	670						
DB	301	AGTCATGAGAAATCAGAGAAATTTGAAGGAGAGCTTTGGAAACATAAAAGGGAAATCAGAAAGG	360						
QY	671	TCATCTGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAGCGGAGCAGGAAAAG	730						
DB	361	TCATCTGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAGCGGAGCAGGAAAAG	420						
QY	731	GACCACTCAGGACCCAGGTGGTGAGCTACAGCAGAGAGGAGCAGCTGTTGGGCATC	790						
DB	421	GACCACTCAGGACCCAGGTGGTGAGCTACAGCAGAGAGGAGCAGCTGTTGGGCATC	480						
QY	791	GTGCTCTGAACCTGAGCTCAAGCTGAACCTCCAGCGGCTCTCTCAGAAATTCCTTTGTTGAA	850						
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QY	851	ATTAGGATGGCTGAAGGAGAGCAGAGGCTAGTAAAGAAATCAAGCATAGTCTCTGGG	910						
DB	541	ATTAGGATGGCTGAAGGAGAGCAGAGGCTAGTAAAGAAATCAAGCATAGTCTCTGGG	600						

QY 911 CCCACGAGAACAGTCTCCACTGCGACGGCATTTGCTTAAATATATAGGACGAGATCTGCAGAT 970  
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QY 1031 AGGGAAGGGGAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGGAGGCCAAAGAAAGA 1090  
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QY 1931 GACAGGACTTGGCGGCAACAGCGGAATATTCGGAATTCATTCCTGCCCAAGTGTGGAGAG 1990  
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QY 1991 GTTCTGCTGACATAGACAGTTACAGATTCACGTGATGGATTGCATCATTTAA 2044  
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Db 1681 GTTCTGCTGACATAGACACGTTACAGATTACGTTGATTCATCATTTAA 1734  
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RESULT 19  
ABX97629

ID ABX97629 standard; cDNA; 1908 BP.

XX AC ABX97629;

XX 16-MAY-2003 (first entry)

XX cDNA encoding novel human protein NOV30b.

DE Human; NOV; adrenoleukodystrophy; congenital adrenal hyperplasia;  
XX haemophilia; hypercoagulation; autoimmune disease; allergy;  
KW immunodeficiency; transplantation; Von Hippel-Lindau syndrome;  
KW Alzheimer's disease; stroke; tuberculous sclerosis; hypercalcaemia;  
KW Parkinson's disease; Huntington's disease; cancer; fertility; diabetes;  
KW adult respiratory distress syndrome; infection; tissue typing;  
KW forensic identification; gene; ss.

XX Homo sapiens.

XX WO200290500-A2.

XX 14-NOV-2002.

XX 02-MAY-2002; 2002WO-US014256.

XX 03-MAY-2001; 2001US-0288395P.

PR 07-MAY-2001; 2001US-0289087P.

PR 08-MAY-2001; 2001US-0289619P.

PR 09-MAY-2001; 2001US-0289817P.

PR 09-MAY-2001; 2001US-0289818P.

PR 11-MAY-2001; 2001US-0290194P.

PR 14-MAY-2001; 2001US-0290753P.

PR 15-MAY-2001; 2001US-0291189P.

PR 21-MAY-2001; 2001US-0292374P.

PR 23-MAY-2001; 2001US-0293107P.

PR 25-MAY-2001; 2001US-0293747P.

PR 29-MAY-2001; 2001US-0294110P.

PR 30-MAY-2001; 2001US-0294434P.

PR 10-SEP-2001; 2001US-0318346P.

PR 17-SEP-2001; 2001US-0322646P.

01-MAY-2002; 2002US-00136728.

(CURA-) CURAGEN CORP.

XX Spytek KA, Li L, Edinger SR, Stone DJ, Guo X, Anderson DW;

PI Patturajan M, Gerlach VL, Taupier RJ, Pena CEA, Padigaru M;

PI Kekuda R, Gorman L, Zerhusen BD, Smithson G, Macdougall JR;

PI Mezes PS, Peyman JA, Zhong M;

XX WFI; 2003-103511/09.

DR P-PSDB; AB065254.

XX New NOVX polypeptides and polynucleotides useful for treating or

PT preventing e.g. congenital adrenal hyperplasia, hemophilia,

PT hypercoagulation, autoimmune disease, allergies, immunodeficiencies,

PT transplantation.

XX Claim 1; Page 163; 300pp; English.

XX The invention describes an isolated polypeptide, NOVX, comprising a

CC sequence or a mature form of one of 21 51-1543 residue amino acid

CC sequences (p1-221), given in the specification. The NOVX polypeptides,

CC polynucleotides and antibodies are useful in the manufacture of a

CC medicament for treating or preventing e.g. adrenoleukodystrophy,

CC congenital adrenal hyperplasia, haemophilia, hypercoagulation, autoimmune

CC disease, allergies, immunodeficiencies, transplantation, Von Hippel-

CC Lindau syndrome, Alzheimer's disease, stroke, tuberculous sclerosis,

CC hypercalcaemia, Parkinson's disease, Huntington's disease, cancer,

CC fertility, diabetes, adult respiratory distress syndrome, viral,  
CC bacterial and parasitic infections. The nucleic acid sequences may be  
CC used in chromosome mapping, identifying individual from minute biological  
CC samples (tissue typing), and in forensic identification of a biological  
CC sample. This sequence encodes a novel human protein (NOV)  
XX  
XX  
SQ Sequence 1908 BP; 637 A; 376 C; 505 G; 390 T; 0 U; 0 Other;

Query Match 81.3%; Score 1688.8; DB 8; Length 1908;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1693; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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QY 438 AGATGAAGAGCTCTGACCAAGAACACACAGCTGAAAGAGCCATGAAGCTTAATAATC 497  
DB 110 AGATGAAGAGCTCTGACCAAGAACACACAGCTGAAAGAGCCATGAAGCTTAATAATC 169  
QY 498 AAGCCATGAAGAGGAGATTTGAGGAGCTTTCCGCTCGACAGAGAAACAGAGGAAGAAC 557  
DB 170 AAGCCATGAAGAGGAGATTTGAGGAGCTTTCCGCTCGACAGAGAAACAGAGGAAGAAC 229  
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QY 798 AACTGCACTCAAGCTCAAGCTCAGCGGCTCCTCAGAGATTCCTTTGTTGAATTAGGA 857  
DB 470 AACTGCACTCAAGCTCAAGCTCAGCGGCTCCTCAGAGATTCCTTTGTTGAATTAGGA 529  
QY 858 TGGCTGAAGGAGAGCAGAGGGTCACTAAAGAAATCAAGCATAGTCTCTGGGCCACGA 917  
DB 530 TGGCTGAAGGAGAGCAGAGGGTCACTAAAGAAATCAAGCATAGTCTCTGGGCCACGA 589  
QY 918 GAACAGTCTCACTGGCAAGCAATGCTTAATATAGGAGCAGATCTGCAGATGGGGCCA 977  
DB 590 GAACAGTCTCACTGGCAAGCAATGCTTAATATAGGAGCAGATCTGCAGATGGGGCCA 649  
QY 978 AGAATTAATTCAGATGAGAGTAACTGTGAGCAGCTCCTGCTGTGCTTAAGGAAG 1037  
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QY 1038 GGAATCAGAAGTGGAGAGCTTCAAGTTCAGCTCAAGAGGCCCCAAAGAAAGCTTTTCA 1097  
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DB 770 ATTTGAAAAGAAACAAAGTAATCGTTCTGAGATTTGAAACCCAGACAGAGGGGAGCAG 829  
QY 1158 AGAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGAAGCACTGA 1217  
DB 830 AGAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGAAGCACTGA 889  
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DB 950 CTGAGCTAATCAAGAGAGACTTCAAGAAAGTGTGAGGCCCTTGAAGGAAAAATTTCTG 1009  
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DB 1130 AGTCCAAATTAATCTGCTCAGATGACACAAACAAAGCTTTCTTCAAGAAACATTAATATG 1189  
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QY 1578 TGAAGGAACCTGAGTGAAGAACTGGAACTGGCAGAGAAAGGCTCTGGCTTCCAAAACAGGTGC 1637  
DB 1250 TGAAGGAACCTGAGTGAAGAACTGGAACTGGCAGAGAAAGGCTCTGGCTTCCAAAACAGGTGC 1309  
QY 1638 AATGAGATGAATGAAGCAAAACCATTCGCCAAGCAGAGAGGAGCCTGGAAAACCATGACCA 1697  
DB 1310 AATGAGATGAATGAAGCAAAACCATTCGCCAAGCAGAGAGGAGCCTGGAAAACCATGACCA 1369  
QY 1698 TCCTCAGGCTCAGATGAGAAAGTTCATGTTCTGATTTTCTGCTGAAAGAGCAGCGAGAG 1757  
DB 1370 TCCTCAGGCTCAGATGAGAAAGTTCATGTTCTGATTTTCTGCTGAAAGAGCAGCGAGAG 1429  
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DB 1430 AGAAATTCATGAGGAAAAAGAGCAACTGGCACTTGCAGCTGGCAAGTTCCTGCTGAAAAGAGA 1489  
QY 1818 ATGATGCTTTTCAAGACGAGAGGAGGAGGAGTCTTGTGATGAGAGATGACAGATGCTCATGGG 1877  
DB 1490 ATGATGCTTTTCAAGACGAGAGGAGGAGGAGTCTTGTGATGAGAGATGACAGATGCTCATGGG 1549  
QY 1878 CGAAGCAAGTGAAGTCTGACCAAGGAGGCTTACCTGTTTCAAGAGGAGCTGAGGACAGGG 1937  
DB 1550 CGAAGCAAGTGAAGTCTGACCAAGGAGGCTTACCTGTTTCAAGAGGAGCTGAGGACAGGG 1609  
QY 1938 ACTGGGGCAACAGCGGAATATTCAGATTCATTCCTGCCCAAGTGTGGAGAGGTTCTGC 1997  
DB 1610 ACTGGGGCAACAGCGGAATATTCAGATTCATTCCTGCCCAAGTGTGGAGAGGTTCTGC 1669  
QY 1998 CTGACATGACAGCTTACAGATTCAGATGATGAGATGTCATCATTTAAGTGTGATGATC 2057  
DB 1670 CTGACATGACAGCTTACAGATTCAGATGATGAGATGTCATCATTTAAGTGTGATGATC 1729  
QY 2058 ACCTCCCAAAACCTGTTGGT 2077  
DB 1730 ACCTCCCAAAACCTGTTGGT 1749

RESULT 20

ACD19488  
ID ACD19488 standard; cdna; 1908 BP.  
XX  
XX ACD19488;  
XX  
XX 25-AUG-2003 (first entry)  
XX  
XX cdna encoding novel human protein #168.  
DE Human; NOV; gene therapy; endocrine related disease; diabetes;  
KW metabolism-related disease; obesity; central nervous system disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;

KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
KW stroke; infection; gene; ss.  
XX Homo sapiens.  
XX WO2003023002-A2.  
XX 20-MAR-2003.  
XX 09-SEP-2002; 2002WO-US028539.  
XX 07-SEP-2001; 2001US-0318120P.  
XX 07-SEP-2001; 2001US-0318130P.  
XX 10-SEP-2001; 2001US-0318430P.  
XX 17-SEP-2001; 2001US-0322636P.  
XX 17-SEP-2001; 2001US-0322781P.  
XX 17-SEP-2001; 2001US-0322816P.  
XX 17-SEP-2001; 2001US-0322817P.  
XX 19-SEP-2001; 2001US-0323519P.  
XX 20-SEP-2001; 2001US-0323631P.  
XX 20-SEP-2001; 2001US-0323636P.  
XX 25-SEP-2001; 2001US-0324969P.  
XX 25-SEP-2001; 2001US-0325051P.  
XX 26-SEP-2001; 2001US-0324990P.  
XX 17-APR-2002; 2002US-0373212P.  
XX 06-SEP-2002; 2002US-00236177.  
XX (CURA-) CURAGEN CORP.  
XX Spytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;  
XX Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;  
XX Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
XX Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigar M, Alsobrook JP;  
XX Lepley DM, Edinger SR, Burgess CE;  
XX WPI; 2003-313242/30.  
XX P-PSDB; ABO14795.  
XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
XX and polynucleotides, useful in gene therapy, e.g. for treating or  
XX preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
XX stroke or infections.  
XX Claim 20; Page 435-436; 586pp; English.  
XX The invention describes a new isolated polypeptide (NOVX). The NOVX  
XX polypeptide, nucleic acid and antibody are useful as therapeutics,  
XX particularly in the manufacture of a medicament for treating a syndrome  
XX associated with a human disease, which includes a pathology associated  
XX with NOVX polypeptide. The DNA encoding the protein is useful in gene  
XX therapy for treating the disease or condition. In particular, the NOVX  
XX polypeptide or polynucleotide is useful for treating endocrine/  
XX metabolism-related diseases (e.g. obesity or diabetes), central nervous  
XX system disorders (e.g. Alzheimer's disease, Parkinson's disease,  
XX epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune  
XX and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,  
XX asthma, inflammatory bowel disease, rheumatoid arthritis or  
XX osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,  
XX prostate or brain cancers, or melanoma), liver diseases (e.g. liver  
XX cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),  
XX haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).  
XX These are also useful in developing powerful assay system for functional  
XX analysis of various human disorders, as well as in diagnostic  
XX applications, and for monitoring the effects of drugs during clinical  
XX trials. This sequence encodes a novel human NOV protein  
XX  
XX Sequence 1908 BP; 637 A; 376 C; 505 G; 390 T; 0 U; 0 Other;  
Query Match 81.3%; Score 1688.8; DB 10; Length 1908;  
Best Local Similarity 99.6%; Pred. No. 0;  
Matches 1693; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 378 GACCCCCCACTGCGCCACCAACCTGGACACGCTTTACCCCGAGGAGCTGCTGCAGC 437  
DB 50 GATCTCCCACTGGATCTCCCAACCTGGACACGCTTTACCCCGAGGAGCTGCTGCAGC 109  
QY 438 AGATGAAGAGAGCTCTCTGACCAAGAACCAACAGCTCTGAAGAGCCATGAAGCTAAATAATC 497  
DB 110 AGATGAAGAGAGCTCTCTGACCGAGAACCAACAGCTCTGAAGAGCCATGAAGCTAAATAATC 169  
QY 498 AAGCCATGAAGAGGAGATTTGAGGAGCTTTGCGCTGGACAGAGAAACAGAGAGGAAGAAC 557  
DB 170 AAGCCATGAAGAGGAGATTTGAGGAGCTTTGCGCTGGACAGAGAAACAGAGAGGAAGAAC 229  
QY 558 GCCAGTTTTTCAGATACAGAGCAAGCAAGAGAGCGCTCTAATGGCCTTGAGTCATG 617  
DB 230 GCCAGTTTTTCAGATACAGAGCAAGCAAGAGAGCGCTCTAATGGCCTTGAGTCATG 289  
QY 618 AGAATGAGAAATTTGAAGGAGAGCTTTGGAATACTAAAGGGGAAATCAGAAAGGTCAATCTG 677  
DB 290 AGAATGAGAAATTTGAAGGAGAGCTTTGGAATACTAAAGGGGAAATCAGAAAGGTCAATCTG 349  
QY 678 AGGACCCCACTGATCACTCAGGCTTCCAGGGCCGAAAGCGAGCAGAGAAAGGACAGC 737  
DB 350 AGGACCCCACTGATCACTCAGGCTTCCAGGGCCGAAAGCGAGCAGAGAAAGGACAGC 409  
QY 738 TCAGGACCCAGGTGAGGCTTACAGCAGAGAGAGCGACCTGTTGGGCATCGTCTG 797  
DB 410 TCAGGACCCAGGTGAGGCTTACAGCAGAGAGAGCGACCTGTTGGGCATCGTCTG 469  
QY 798 AACTGCAGCTCAAGCTGAACTCCAGCGGCTCCCTCAGAAGATTCCTTTGTTGAAATTAGGA 857  
DB 470 AACTGCAGCTCAAGCTGAACTCCAGCGGCTCCCTCAGAAGATTCCTTTGTTGAAATTAGGA 529  
QY 858 TGGCTGAAGAGAGAGCAGAGAGGTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCACAGA 917  
DB 530 TGGCTGAAGAGAGAGCAGAGAGGTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCACAGA 589  
QY 918 GAACAGTCTCCACTGGCAGCGCATTTGCTAAATATATAGGAGCAGATCTGCAGATGGGGCCA 977  
DB 590 GAACAGTCTCCACTGGCAGCGCATTTGCTAAATATATAGGAGCAGATCTGCAGATGGGGCCA 649  
QY 978 AGAATTAATTCGAAATCATGAGGAGTTAACTGTGAGCCAGCTCTCTGCTGTGCTAAGGGAAG 1037  
DB 650 AGAATTAATTCGAAATCATGAGGAGTTAACTGTGAGCCAGCTCTCTGCTGTGCTAAGGGAAG 709  
QY 1038 GGAATCAGAAGGTGGAGAGACTTGAAGTTGCACTCAAGAGAGGCCAAAGAAAGTTTCAG 1097  
DB 710 GGAATCAGAAGGTGGAGAGACTTGAAGTTGCACTCAAGAGAGGCCAAAGAAAGTTTCAG 769  
QY 1098 ATTTTGAAGAGAGAGAGAGTCTGTTCTGAGATTGAAACCCAGAGAGGGGAGCAGCAG 1157  
DB 770 ATTTTGAAGAGAGAGAGAGTCTGTTCTGAGATTGAAACCCAGAGAGGGGAGCAGCAG 829  
QY 1158 AGAAGAGAGATGATGAAGAGAGAGGCGCCGAGAGCTGTGGAAGCGAAGTGGAAAGCACTGA 1217  
DB 830 AGAAGAGAGATGATGAAGAGAGAGGCGCCGAGAGCTGTGGAAGCGAAGTGGAAAGCACTGA 889  
QY 1218 ACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTTCAAAAATCAGAGCAAG 1277  
DB 890 ACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTTCAAAAATCAGAGCAAG 949  
QY 1278 CTGAGCTAATGAGAGAGAGCTTCAAGAAAGTTCAGGCCCTTGAAGGAAATTTCTG 1337  
DB 950 CTGAGCTAATGAGAGAGAGCTTCAAGAAAGTGTGAGGCCCTTGAAGGAAATTTCTG 1009  
QY 1338 CAATTCATCAGAGTTGAATGAAAGCAGAGCTTGTATTACTACTAAACAAAGTTAGAGC 1397  
DB 1010 CAATTCATCAGAGTTGAATGAAAGCAGAGCTTGTATTACTACTAAACAAAGTTAGAGC 1069  
QY 1398 TACAAGTGAAGAGAGCTTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAA 1457  
DB 1070 TACAAGTGAAGAGAGCTTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAA 1129  
QY 1458 AGTCCAAATTAATCTGTGCTACAGATGACACACAAAGCTTCTTCAAGAAATAATAATG 1517

Db 1130 AGTCAAATTAACGTGTGTCAGATGACACACAAAGCTTCTTCAAGAAATATAATG 1189  
Qy 1518 CATTGAAAAAATTTGAGGAACTTAACAAGAAAAAGAGTCAGAAAAAGTGGACAGGGCAGTGC 1577  
Db 1190 CATTGAAAAAATTTGAGGAACTTAACAAGAAAAAGAGTCAGAAAAAGTGGACAGGGCAGTGC 1249  
Qy 1578 TGAAGGAACTGAGTGAAGAACTGGAATGCGGAGAGAGGCTCTGGCTTCCAAAACAGTGC 1637  
Db 1250 TGAAGGAACTGAGTGAAGAACTGGAATGCGGAGAGAGGCTCTGGCTTCCAAAACAGTGC 1309  
Qy 1638 AAATGGATGAATGAAGCAACCAATTCGAAGCAGGAGAGGACTGGAAACCATGACCA 1697  
Db 1310 AAATGGATGAATGAAGCAACCAATTCGAAGCAGGAGAGGACTGGAAACCATGACCA 1369  
Qy 1698 TCCTCAGGGCTCAGATGGAAGTTTACTGTCTTCTGATTTTTCATGCTGAAAGAGCAGCGAGAG 1757  
Db 1370 TCCTCAGGGCTCAGATGGAAGTTTACTGTCTTCTGATTTTTCATGCTGAAAGAGCAGCGAGAG 1429  
Qy 1758 AGAAATTCATGAGGAAAGAGCAACTGGCAATTCGAGCTGGCAGTCTGCTGAAAGAGA 1817  
Db 1430 AGAAATTCATGAGGAAAGAGCAACTGGCAATTCGAGCTGGCAGTCTGCTGAAAGAGA 1489  
Qy 1818 ATGATGCTTTCGAAGACGGAGCAGGAGTCTTGTGATGGAGATCAGAGTCTCATGGG 1877  
Db 1490 ATGATGCTTTCGAAGACGGAGCAGGAGTCTTGTGATGGAGATCAGAGTCTCATGGG 1549  
Qy 1878 CGAAGCAAGTGAATCTGACAGCAGGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGG 1937  
Db 1550 CGAAGCAAGTGAATCTGACAGCAGGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGG 1609  
Qy 1938 ACTGGCGCAACAGCGGAATATTCGATTCATCTCTGCCCCCAAGTGTGGAGAGTTCCTGC 1997  
Db 1610 ACTGGCGCAACAGCGGAATATTCGATTCATCTCTGCCCCCAAGTGTGGAGAGTTCCTGC 1669  
Qy 1998 CTGACATAGACAGCTTACAGATTCACGTGATGGATTCATCAATTAAGTGTGATGATC 2057  
Db 1670 CTGACATAGACAGCTTACAGATTCACGTGATGGATTCATCAATTAAGTGTGATGATC 1729  
Qy 2058 ACCTTCCCCAAAACCTGTTGGT 2077  
Db 1730 ACCTTCCCCAAAACCTGTTGGT 1749  
RESULT 21  
ACD19486  
ID ACD19486 standard; cDNA; 1858 BP.  
XX AC ACD19486;  
XX  
XX 25-AUG-2003 (first entry)  
XX cDNA encoding novel human protein #166.  
XX Human; NOV; gene therapy; endocrine related disease; diabetes;  
KW metabolism-related disease; obesity; central nervous system disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
KW stroke; infection; gene; ss.  
XX  
OS Homo sapiens.  
XX  
XX WO2003023002-A2.  
XX  
XX 20-MAR-2003.  
XX  
XX 09-SEP-2002; 2002WO-US028539.  
XX  
XX

PR 07-SEP-2001; 2001US-0318120P.  
PR 10-SEP-2001; 2001US-0318130P.  
PR 10-SEP-2001; 2001US-0318430P.  
PR 17-SEP-2001; 2001US-0322636P.  
PR 17-SEP-2001; 2001US-0322781P.  
PR 17-SEP-2001; 2001US-0322816P.  
PR 17-SEP-2001; 2001US-0322817P.  
PR 19-SEP-2001; 2001US-0323519P.  
PR 20-SEP-2001; 2001US-0323631P.  
PR 20-SEP-2001; 2001US-0323636P.  
PR 25-SEP-2001; 2001US-0324969P.  
PR 25-SEP-2001; 2001US-0325091P.  
PR 26-SEP-2001; 2001US-0324990P.  
PR 17-SEP-2002; 2002US-0373212P.  
PR 06-SEP-2002; 2002US-00236177.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Szytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M,  
PI Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;  
PI Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigaru M, Alsobrook JP;  
PI Lepley DM, Edinger SR, Burgess CE;  
XX  
XX WPI; 2003-313242/30.  
DR P-PSDB; ABO14793.  
XX  
XX New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
PT and polynucleotides, useful in gene therapy, e.g. for treating or  
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
PT stroke or infections.  
XX  
XX Claim 20; Page 434; 586pp; English.  
XX  
XX The invention describes a new isolated polypeptide (NOVX). The NOVX  
CC polypeptide, nucleic acid and antibody are useful as therapeutics,  
CC particularly in the manufacture of a medicament for treating a syndrome  
CC associated with a human disease, which includes a pathology associated  
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene  
CC therapy for treating the disease or condition. In particular, the NOVX  
CC polypeptide or polynucleotide is useful for treating endocrine/  
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous  
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,  
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune  
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,  
CC asthma, inflammatory bowel disease, rheumatoid arthritis or  
CC osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,  
CC prostate or brain cancers, or melanoma), liver diseases (e.g. liver  
CC cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),  
CC haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).  
CC These are also useful in developing powerful assay system for functional  
CC analysis of various human disorders, as well as in diagnostic  
CC applications, and for monitoring the effects of drugs during clinical  
CC trials. This sequence encodes a novel human NOV protein  
XX  
XX SQ Sequence 1858 BP; 624 A; 360 C; 497 G; 377 T; 0 U; 0 Other;  
Query Match 81.3%; Score 1687.8; DB 10; Length 1858;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 1692; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
Qy 379 ACCCCCCCACTGGCCCCCACCACCACTGGACAGCTTTACCCCGAGGAGCTGTGCAGCA 438  
Db 1 ATCTCTCCACCTGGATCTCCCAAACTGGACAGCTTTACCCCGAGGAGCTGTGCAGCA 60  
Qy 439 GATGAAAGAGCTCTTGACCAAGAACCAACCAGCTGAAAGAGCCATGAATTAATCA 498  
Db 61 GATGAAAGAGCTCTTGACCAAGAACCAACCAGCTGAAAGAGCCATGAATTAATCA 120  
Qy 499 AGCCATGAAGGAGGATTTGAGGAGCTTTTCGGCTTGGACAGAGAAACAGAGGAGAACG 558  
Db 121 AGCCATGAAGGAGGATTTGAGGAGCTTTTCGGCTTGGACAGAGAAACAGAGGAGAACG 180



QY	559	CCAGTTTTTTTGATACAGAGCAAGAAAGAGCGCTTAATGCGCTTGAGTCATGA	618	Db	1261	AATGATGAATGAAGCAAAACCATTTGCCAAGCAGGAAGGACCTTGGAAACCATGACCAT	1320
Db	181	CCAGTTTTTTTGATACAGAGCAAGAAAGAGCGCTTAATGCGCTTGAGTCATGA	240	QY	1699	CCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGACGACGAGAGA	1758
QY	619	GAATGAGAAATTGAAGGAGAGCTTGGAAATCTAAAGGGGAATCAGAAAGTCTCTGA	678	Db	1321	CCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGACGACGAGAGA	1380
Db	241	GAATGAGAAATTGAAGGAGAGCTTGGAAATCTAAAGGGGAATCAGAAAGTCTCTGA	300	QY	1759	GAAATTTTCATGAGGAAAAAGGACAACTGGCATTGCACTGGCAGTTTCTGCTGAAAGAGAA	1818
QY	679	GGACCCCACTGATGACTCCAGGGCTTCCAGGGCCGGAAGCGGACAGCAAAAGACCAAGCT	738	Db	1381	GAAATTTTCATGAGGAAAAAGGACAACTGGCATTGCACTGGCAGTTTCTGCTGAAAGAGAA	1440
Db	301	GGACCCCACTGATGACTCCAGGGCTTCCAGGGCCGGAAGCGGACAGCAAAAGACCAAGCT	360	QY	1819	TGATGCTTTTCGAAAGCGGAGCAGCAGTCCTTGTGATGGAGATGCAGAGTCGTCATCGGGC	1878
QY	739	CAGGACCCAGGTGGTGAAGGCTACAAGCAGAGAGAGGACACCTGTTTGGGCATCGTGTCTGA	798	Db	1441	TGATGCTTTTCGAAAGCGGAGCAGCAGTCCTTGTGATGGAGATGCAGAGTCGTCATCGGGC	1500
Db	361	CAGGACCCAGGTGGTGAAGGCTACAAGCAGAGAGAGGACACCTGTTTGGGCATCGTGTCTGA	420	QY	1879	GAGAACAGTGACTCTGACCAGCAGGCTTACCTTGTTCAAAAGAGGAGCTGAGACACAGGA	1938
QY	799	ACTGCAAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATTCTTTGTTGAAATTAGGAT	858	Db	1501	GAGAACAGTGACTCTGACCAGCAGGCTTACCTTGTTCAAAAGAGGAGCTGAGACACAGGA	1560
Db	421	ACTGCAAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATTCTTTGTTGAAATTAGGAT	480	QY	1939	CTGGCGGCAACAGCGGAATATTCCGATTCACTTCCTGCCCAAGTGTGGAGAGGTTCTGCC	1998
QY	859	GGCTGAAGGAGAGCAGAGGCTCAGTAAAGAAATCAAGCATAGTCCTGGGCCACAGAG	918	Db	1561	CTGGCGGCAACAGCGGAATATTCCGATTCACTTCCTGCCCAAGTGTGGAGAGGTTCTGCC	1620
Db	481	GGCTGAAGGAGAGCAGAGGCTCAGTAAAGAAATCAAGCATAGTCCTGGGCCACAGAG	540	QY	1999	TGACATAGACACGTTTACAGATTCACTGATGGATTGTCATCATTTTAAGTGTGATGATATCA	2058
QY	919	AACAGTCTCCACTGGCACGGCATTTGTCTAAATATAGGAGCAGATCTGCAAGTGGGCCAA	978	Db	1621	TGACATAGACACGTTTACAGATTCACTGATGGATTGTCATCATTTTAAGTGTGATGATATCA	1680
Db	541	AACAGTCTCCACTGGCACGGCATTTGTCTAAATATAGGAGCAGATCTGCAAGTGGGCCAA	600	QY	2059	CCTCCCCCAAACTGTTGGT 2077	
QY	979	GAATTAATTCGAAATGAGAGGTTAACTGTGAGCCAGCTCTCTGCTGCTTAAGGAAGG	1038	Db	1681	CCTCCCCCAAACTGTTGGT 1699	
Db	601	GAATTAATTCGAAATGAGAGGTTAACTGTGAGCCAGCTCTCTGCTGCTTAAGGAAGG	660	RESULT 22			
QY	1039	GAATCAGAGGTGGAGAGCTTCAAGTTGCACTCAAGGAGGCCAAAGAAAGAGTTTCAGA	1098	ID	ABX97628		
Db	661	GAATCAGAGGTGGAGAGCTTCAAGTTGCACTCAAGGAGGCCAAAGAAAGAGTTTCAGA	720	XX	ABX97628 standard; cDNA; 1908 BP.		
QY	1099	TTTTTGAAGAAACCAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAGA	1158	AC	ABX97628;		
Db	721	TTTTTGAAGAAACCAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAGA	780	XX			
QY	1159	GAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGAACACTGAA	1218	DT	16-MAY-2003 (first entry)		
Db	781	GAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGAACACTGAA	840	XX	cDNA encoding novel human protein NOV30a.		
QY	1219	CCTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC	1278	DE	Human; NOV; adrenoleukodystrophy; congenital adrenal hyperplasia;		
Db	841	CCTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC	900	XX	haemophilia; hypercoagulation; autoimmune disease; allergy;		
QY	1279	TGAGCTAATGAAGAGAGACTTCAAGAAAAAGTGTGAGGCCCTTGAAGGAAAAATTCTGC	1338	KW	immunodeficiency; transplantation; Von Hippel-Lindau syndrome;		
Db	901	TGAGCTAATGAAGAGAGACTTCAAGAAAAAGTGTGAGGCCCTTGAAGGAAAAATTCTGC	960	KW	Alzheimer's disease; stroke; tuberosus sclerosis; hypercalcaemia;		
QY	1339	AATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTGTTTATCTAAACAAAAGTTAGAGCT	1398	KW	Parkinson's disease; Huntington's disease; cancer; fertility; diabetes;		
Db	961	AATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTGTTTATCTAAACAAAAGTTAGAGCT	1020	KW	adult respiratory distress syndrome; infection; tissue typing;		
QY	1399	ACAAGTGAAGAGCTATCAGAAATCAAAATGGACAGCTTAAACACAGAGATGAAA	1458	XX	forensic identification; gene; ss.		
Db	1021	ACAAGTGAAGAGCTATCAGAAATCAAAATGGACAGCTTAAACACAGAGATGAAA	1080	OS	Homo sapiens.		
QY	1459	GTCCAAATTAATCTGTCTACAGATGACACACAAACAGCTTCTTCAAGAACATATATATGC	1518	PN	WO200290500-A2.		
Db	1081	GTCCAAATTAATCTGTCTACAGATGACACACAAACAGCTTCTTCAAGAACATATATATGC	1140	XX	14-NOV-2002.		
QY	1519	ATTGAAACCAATTGAGGAACTTAAACAGAAAGAGTCAAGAAAGTGACAGGGCAGTCT	1578	XX	02-MAY-2002; 2002WO-US014256.		
Db	1141	ATTGAAACCAATTGAGGAACTTAAACAGAAAGAGTCAAGAAAGTGACAGGGCAGTCT	1200	XX	03-MAY-2001; 2001US-0288395P.		
QY	1579	GAAGGAACTGAGTCAAAACCTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAAACAGCTGCA	1638	PR	07-MAY-2001; 2001US-0289087P.		
Db	1201	GAAGGAACTGAGTCAAAACCTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAAACAGCTGCA	1260	PR	08-MAY-2001; 2001US-0289619P.		
QY	1639	AATGGATGAATGAAGCAAAACCATTTGCCAAGCAGGAAGAGACCTGGAAACCATGACCAT	1698	PR	09-MAY-2001; 2001US-0289817P.		
				PR	11-MAY-2001; 2001US-0290194P.		
				PR	14-MAY-2001; 2001US-0290753P.		
				PR	15-MAY-2001; 2001US-0291189P.		
				PR	21-MAY-2001; 2001US-0292374P.		
				PR	23-MAY-2001; 2001US-0293107P.		
				PR	25-MAY-2001; 2001US-0293747P.		
				PR	29-MAY-2001; 2001US-0294110P.		
				PR	30-MAY-2001; 2001US-0294434P.		
				PR	10-SEP-2001; 2001US-0318346P.		
				PR	17-SEP-2001; 2001US-0322646P.		

PR 01-MAY-2002; 2002US-00136728.  
XX (CURA-) CURAGEN CORP.  
XX  
XX Spvtek KA, Li L, Edinger SR, Stone DJ, Guo X, Anderson DW;  
PI Patturajan M, Gerlach VL, Taupier RJ, Pena CEA, Padigaru M;  
PI Kekuda R, Gorman L, Zernhusen BU, Smithson G, Macdougall JR;  
PI Mezes PS, Peyman JA, Zhong M;  
XX WPI; 2003-103511/09.  
DR P-PSDB; ABU65253.  
DR  
XX  
XX New NOVX polypeptides and polynucleotides useful for treating or  
PT preventing e.g. congenital adrenal hyperplasia, hemophilia,  
PT hypercoagulation, autoimmune disease, allergies, immunodeficiencies,  
PT transplantation.  
XX  
XX Claim 1; Page 162; 300pp; English.  
XX  
XX The invention describes an isolated polypeptide, NOVX, comprising a  
CC sequence or a mature form of one of 21 51-1543 residue amino acid  
CC sequences (PI-p21), given in the specification. The NOVX polypeptides,  
CC polynucleotides and antibodies are useful in the manufacture of a  
CC medicament for treating or preventing e.g. adrenoleukodystrophy,  
CC congenital adrenal hyperplasia, haemophilia, hypercoagulation, autoimmune  
CC disease, allergies, immunodeficiencies, transplantation, Von Hippel-  
CC Lindau syndrome, Alzheimer's disease, stroke, tuberosus sclerosis,  
CC hypercalcaemia, Parkinson's disease, Huntington's disease, cancer,  
CC fertility, diabetes, adult respiratory distress syndrome, viral,  
CC bacterial, and parasitic infections. The nucleic acid sequences may be  
CC used in chromosome mapping, identifying individual from minute biological  
CC samples (tissue typing), and in forensic identification of a biological  
CC sample. This sequence encodes a novel human protein (NOV)  
XX  
SQ Sequence 1908 BP; 633 A; 380 C; 505 G; 390 T; 0 U; 0 Other;  
  
Query Match 79.3%; Score 1646.6; DB 8; Length 1908;  
Best Local Similarity 98.5%; Pred. No. 0;  
Matches 1674; Conservative 0; Mismatches 7; Indels 18; Gaps 1;  
  
QY 379 ACCCCCCACCTGGCCACCACCAACCTGGACACGTTTACCCCGGAGAGCTGTCGACGA 438  
DB 69 ATCTCTCCACCTGGATCTCCCAACCTGGACACATTTACCCCGGAGAGCTGTCGACGA 128  
  
QY 439 GATGAAGAGAGCTCTGTACCAAGAACACACAGCTGGAAGAGCCATGAAGCTAAATATCA 498  
DB 129 GATGAAGAGAGCTCTGTACCAAGAACACACAGCTGGAAGAGCCATGAAGCTAAATATCA 188  
  
QY 499 AGCCATGAAGAGGAGATTGAGGAGCTTTCCGGCTGGACAGAGAAACAGAGGAAGAACG 558  
DB 189 AGCCATGAAGAGGAGATTGAGGAGCTTTCCGGCTGGACAGAGAAACAGAGGAAGAACG 248  
  
QY 559 CAGATTTTGTAGATACAGAGCAAGAAAGCAAGAGCGTCTAATGGCCCTTGAAGTATGA 618  
DB 249 CAGATTTTGTAGATACAGAGCAAGAAAGCAAGAGCGTCTAATGGCCCTTGAAGTATGA 308  
  
QY 619 GAATGAGAAATTCAGAGAGAGCTTGAAGAACTTAAAGGGAATCAGAAAGTCAATCTGA 678  
DB 309 GAATGAGAAATTCAGAGAGAGCTTGAAGAACTTAAAGGGAATCAGAAAGTCAATCTGA 368  
  
QY 679 GGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCCGGAGAGGAGAAAGACCAAGCT 738  
DB 369 GGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCCGGAGAGGAGAAAGACCAAGCT 428  
  
QY 739 CAGGACCCAGGTGGTGAAGGCTTAAAGCAGAGAGAGGAGACCTGTGTGGCATCTGTCTGA 798  
DB 429 CAGGACCCAGGTGGTGAAGGCTTAAAGCAGAGAGAGGAGACCTGTGTGGCATCTGTCTGA 488  
  
QY 799 ACTGCAAGCTCAAGCTCAAGCTCCAGCGCTCCTCAGAGATTCTCTTTGTAATATTAGAT 858  
DB 489 ACTGCAAGCTCAAGCTCAAGCTCCAGCGCTCCTCAGAGATTCTCTTTGTAATATTAGAT 548  
  
QY 859 GGCTGAAGGAGAGAGAGAGGGTTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCACGAG 918

DB 549 GGCTGAAGGAGAGAGAGGGTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCACGAG 608  
QY  
QY 919 AACAGTCTCAGCTGGCACGGCATTTGTCTAAATATATAGAGAGAGATCTCCAGATGGGGCAA 978  
DB 609 AACAGTCTCAGCTGGCAC-----GAGCAGATCTGCAGATGGGGCAA 650  
QY 979 GAATTAATCTCGAACAATGAGGAGTTAACTGTGAGCCAGCTCCTGCTGTCCCTAAGGGAAGG 1038  
DB 651 GAATTAATCTCGAACAATGAGGAGTTAACTGTGAGCCAGCTCCTGCTGTCCCTAAGGGAAGG 710  
QY 1039 GAATCAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGAGGCGCAAAAGAAAGATTTTCA 1098  
DB 711 GAATCAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGAGGCGCAAAAGAAAGATTTTCA 770  
QY 1099 TTTTGAAGAAAGAAACCAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACA 1158  
DB 771 TTTTGAAGAAAGAAACCAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACA 830  
QY 1159 GAAAGAGAAATGATCAAGAGAGAAAGCGCCGAGAGACTGTTGGAAGCGAAGTGGAAAGCACTGAA 1218  
DB 831 GAAAGAGAAATGATCAAGAGAGAAAGCGCCGAGAGACTGTTGGAAGCGAAGTGGAAAGCACTGAA 890  
QY 1219 CCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC 1278  
DB 891 CCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC 950  
QY 1279 TGAGCTTAATGAAGAGAGACTTCAAGAAAGTCTCAGGCCCTTGAAGGAAAGAAATTTCTGC 1338  
DB 951 TGAGCTTAATGAAGAGAGACTTCAAGAAAGTCTCAGGCCCTTGAAGGAAAGAAATTTCTGC 1010  
QY 1339 AATTCATCAGAGCTGCAATGAAAGCAAGAGCTTGTATTATCTAAACAAAAGTTAGAGCT 1398  
DB 1011 AATTCATCAGAGCTTGAATGAAAGCAAGAGCTTGTATTATCTAAACAAAAGTTAGAGCT 1070  
QY 1399 ACAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGATGAAAA 1458  
DB 1071 ACAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGATGAAAA 1130  
QY 1459 GTCCAAATTAATCTGCTACAGATGACACACACACAGCTTCTTCAAGAACATTAATATGC 1518  
DB 1131 GTCCAAATTAATCTGCTACAGATGACACACACACAGCTTCTTCAAGAACATTAATATGC 1190  
QY 1519 ATTGAAAAACAATTTGAGGAACTTCAAGAAAGAGTCAAGAAAAAGTGACAGGCGAGTGTCT 1578  
DB 1191 ATTGAAAAACAATTTGAGGAACTTCAAGAAAGAGTCAAGAAAAAGTGACAGGCGAGTGTCT 1250  
QY 1579 GAAAGAACTCAGTGAAGAAACTTGAACCTGGCAGAGAAAGGCTCTGGCTTCCAAAACAGCTGCA 1638  
DB 1251 GAAAGAACTCAGTGAAGAAACTTGAACCTGGCAGAGAAAGGCTCTGGCTTCCAAAACAGCTGCA 1310  
QY 1639 AATGGATGAAATGAAGCAAAACCAATTCGCAAGCAGGAGAGGACCTGGAACCAATGACCAT 1698  
DB 1311 AATGGATGAAATGAAGCAAAACCAATTCGCAAGCAGGAGAGGACCTGGAACCAATGACCAT 1370  
QY 1699 CCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTGCTGAAAGACGAGAGAGA 1758  
DB 1371 CCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTGCTGAAAGACGAGAGAGA 1430  
QY 1759 GAAATTCATGAGAAAAAGGAGCAACTGGCATTTGCAGCTGGCAGATTTCTGCTGAAAGAGAA 1818  
DB 1431 GAAATTCATGAGAAAAAGGAGCAACTGGCATTTGCAGCTGGCAGATTTCTGCTGAAAGAGAA 1490  
QY 1819 TGATGCTTTTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1878  
DB 1491 TGATGCTTTTGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1550  
QY 1879 GAGAAACAGTGTCTGACAGCAGGCTTACCTGTTGTTTCAAGAGAGGAGGAGGAGGAGGAG 1938  
DB 1551 GAGAAACAGTGTCTGACAGCAGGCTTACCTGTTGTTTCAAGAGAGGAGGAGGAGGAGGAG 1610  
QY 1939 CTGGCGGCAACAGCGGAATATTTCGGATTTCATTCCTGCCCCCAAGTGTGGAGAGGTTCTGCC 1998



Db 711 GAATCAGAGGTGGAGACATTGAAGTTGCACTCAAGGAGGCCAAGAAAGAGTTTTCAGA 770  
Qy TTTTGAAGAAGAAAACAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACAGA 1158  
Db TTTTGAAGAAGAAAACAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACAGA 830  
Qy GAAAGAGATGATGAAGAGAAGGCCCGGAGACTGTTGGAAGCGAAGTGGGAAGCACTGAA 1218  
Db GAAAGAGATGATGAAGAGAAGGCCCGGAGACTGTTGGAAGCGAAGTGGGAAGCACTGAA 890  
Qy CCTCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGGAAGC 1278  
Db CCTCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGGAAGC 950  
Qy TGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCCCTTGAAGGAAAAAATTCGCG 1338  
Db TGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCCCTTGAAGGAAAAAATTCGCG 1010  
Qy AATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTATTATCTAAACAAAAGTTAGAGCT 1398  
Db AATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTATTATCTAAACAAAAGTTAGAGCT 1070  
Qy ARAAGTGAAGAGCATCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAA 1458  
Db ARAAGTGAAGAGCATCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAA 1130  
Qy GTCCAAATTAAGTGTGCTACAGATGACACACAAAGCTTCTCAAGAACATATAATGCG 1518  
Db GTCCAAATTAAGTGTGCTACAGATGACACACAAAGCTTCTCAAGAACATATAATGCG 1190  
Qy ATTGAAAACAAATTGAGGAATTAACAAGAAAAGAGTCAGAAAAGTGGACAGGCGAGTGC 1578  
Db ATTGAAAACAAATTGAGGAATTAACAAGAAAAGAGTCAGAAAAGTGGACAGGCGAGTGC 1250  
Qy GAAGGAACCTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCA 1638  
Db GAAGGAACCTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCA 1310  
Qy AATGGATGAATGAAGCAAAACCATTCGCAAGCAGAGAGGACCTGGAAACCATGACCAT 1698  
Db AATGGATGAATGAAGCAAAACCATTCGCAAGCAGAGAGGACCTGGAAACCATGACCAT 1370  
Qy CCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGAGCAGCAGAGA 1758  
Db CCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGAGCAGCAGAGA 1430  
Qy GAAATTCATGAGAAAAGGAGCACTGGCAATTCGAGCTGGCAGTTCTGCTGAAAGAGAA 1818  
Db GAAATTCATGAGAAAAGGAGCACTGGCAATTCGAGCTGGCAGTTCTGCTGAAAGAGAA 1490  
Qy TGATGCTTTTGAAGCAGGAGCGGAGTCTTCTGATGGAGATCAGAGTCTGATGGGC 1878  
Db TGATGCTTTTGAAGCAGGAGCGGAGTCTTCTGATGGAGATCAGAGTCTGATGGGC 1550  
Qy GAGAACAGTGACTCTGACCAAGAGGCTTACTTGTTCAAAGAGGAGCTGAGGACAGGGA 1938  
Db GAGAACAGTGACTCTGACCAAGAGGCTTACTTGTTCAAAGAGGAGCTGAGGACAGGGA 1610  
Qy CTGGCGGCAACAGCGGAATATTCGATTCATCTGCCCCCAAGTGTGGAGAGGTTCTGCC 1998  
Db CTGGCGGCAACAGCGGAATATTCGATTCATCTGCCCCCAAGTGTGGAGAGGTTCTGCC 1670  
Qy TGACATAGACAGCTTACAGATTCACGTGATGATTCATATTAAGTTGATGATCA 2058  
Db TGACATAGACAGCTTACAGATTCACGTGATGATTCATATTAAGTTGATGATCA 1730  
Qy CCTCCCCAAAACCTGTGGT 2077  
Db CCTCCCCAAAACCTGTGGT 1749

ACD19487  
ID ACD19487 standard; cDNA; 1857 BP.  
XX  
AC ACD19487;  
XX  
DT 25-AUG-2003 (first entry)  
XX  
DE cDNA encoding novel human protein #167.  
XX  
KW Human; NOV; gene therapy; endocrine related disease; diabetes;  
KW metabolism-related disease; obesity; central nervous system disorder;  
KW Alzheimer's disease; Parkinson's disease; epilepsy; multiple sclerosis;  
KW schizophrenia; depression; autoimmune disorder; inflammatory disorder;  
KW psoriasis; allergy; lupus erythematosus; asthma; cancer;  
KW inflammatory bowel disease; rheumatoid arthritis; osteoarthritis;  
KW colon cancer; lung cancer; liver cancer; breast cancer; ovarian cancer;  
KW prostate cancer; brain cancer; melanoma; liver disease; liver cirrhosis;  
KW lung disease; emphysema; obstructive pulmonary disease; haemophilia;  
KW stroke; infection; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2003023002-A2.  
XX  
PD 20-MAR-2003.  
XX  
PF 09-SEP-2002; 2002WO-US028539.  
XX  
PR 07-SEP-2001; 2001US-0318120P.  
PR 07-SEP-2001; 2001US-0318130P.  
PR 10-SEP-2001; 2001US-0318430P.  
PR 17-SEP-2001; 2001US-0322636P.  
PR 17-SEP-2001; 2001US-0322781P.  
PR 17-SEP-2001; 2001US-0322816P.  
PR 17-SEP-2001; 2001US-0322817P.  
PR 19-SEP-2001; 2001US-0323519P.  
PR 20-SEP-2001; 2001US-0323631P.  
PR 20-SEP-2001; 2001US-0323636P.  
PR 25-SEP-2001; 2001US-0324969P.  
PR 25-SEP-2001; 2001US-0325091P.  
PR 26-SEP-2001; 2001US-0324990P.  
PR 17-APR-2002; 2002US-0373212P.  
PR 06-SEP-2002; 2002US-00236177.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Sytek KA, Patturajan M, Gorman L, Li L, Anderson DW, Zhong M;  
PI Gerlach VL, Vernet CAM, Ellerman K, Berghs C, Rothenberg ME, Guo X;  
PI Shimkets RA, Leach MD, Catterton E, Kekuda R, Ji W, Miller CE;  
PI Rieger DK, Taupier RJ, Shenoy SG, Liu X, Padigar M, Alsobrook JP;  
PI Lepley DM, Edinger SR, Burgess CE;  
XX  
DR WPI; 2003-313242/30.  
DR P-PSDB; ABO14794.  
XX  
PT New cytoplasmic, nuclear membrane bound or secreted polypeptides (NOVX)  
PT and polynucleotides, useful in gene therapy, e.g. for treating or  
PT preventing obesity, multiple sclerosis, allergy, cancers, hemophilia,  
PT stroke or infections.  
XX  
PS Claim 20; Page 435; 586pp; English.  
XX  
CC The invention describes a new isolated polypeptide (NOVX). The NOVX  
CC polypeptide, nucleic acid and antibody are useful as therapeutics,  
CC particularly in the manufacture of a medicament for treating a syndrome  
CC associated with a human disease, which includes a pathology associated  
CC with NOVX polypeptide. The DNA encoding the protein is useful in gene  
CC therapy for treating the disease or condition. In particular, the NOVX  
CC polypeptide or polynucleotide is useful for treating endocrine/  
CC metabolism-related diseases (e.g. obesity or diabetes), central nervous  
CC system disorders (e.g. Alzheimer's disease, Parkinson's disease,  
CC epilepsy, multiple sclerosis, schizophrenia or depression), autoimmune  
CC and inflammatory disorders (e.g. psoriasis, allergy, lupus erythematosus,

CC	asthma, inflammatory bowel disease, rheumatoid arthritis or
CC	osteoarthritis), cancers (e.g. colon, lung, liver, breast, ovarian,
CC	prostate or brain cancers, or melanoma), liver diseases (e.g. liver
CC	cirrhosis), lung diseases (emphysema or obstructive pulmonary disease),
CC	haemophilia, stroke, or infections (e.g. viral, bacterial or parasitic).
CC	These are also useful in developing powerful assay system for functional
CC	analysis of various human disorders, as well as in diagnostic
CC	applications, and for monitoring the effects of drugs during clinical
CC	trials. This sequence encodes a novel human NOV protein
XX	
SQ	Sequence 1857 BP; 620 A; 363 C; 497 G; 377 T; 0 U; 0 Other;
Query Match 79.0%; Score 1641.8; DB 10; Length 1857;	
Best Local Similarity 98.5%; Pred. No. 0;	
Matches 1674; Conservative 0; Mismatches 7; Indels 18; Gaps 1;	
QY	379 ACCCCGCCACCTGGCCCAACCCCAACCTGGACACGTTTACCCCGAGAGCTGCTGCAGCA 438
DB	18 ATCCTCCCACTGGATCTCCCAACCTGGACACATTTACCCCGAGAGCTGCTGCAGCA 77
QY	439 GATGAAGAGCTCCTGACCAAGAACCAACACAGCTGAAAGAGCCATGAAGCTAAATATCA 498
DB	78 GATGAAGAGCTCCTGACCGAGAACCAACAGCTGAAAGAGCCATGAAGCTAAATATCA 137
QY	499 AGCCATGAAGGAGATTGTGAGAGCTTTCGGCTCGGACAGAGAAACAGAGGAAGACG 558
DB	138 AGCCATGAAGGAGATTGTGAGAGCTTTCGGCTCGGACAGAGAAACAGAGGAAGACG 197
QY	559 CCAAGTTTTTGATACAGACGACAAAGACCAAGAGCGCTTAATGGCTTGAGTCATGA 618
DB	198 CCAAGTTTTTGATACAGACGACAAAGACCAAGAGCGCTTAATGGCTTGAGTCATGA 257
QY	619 GAATGAGAAATTCGAAGAGAGCTTGGAAATTCGAAGGAAATTCGAAGAGTCATCTGA 678
DB	258 GAATGAGAAATTCGAAGAGAGCTTGGAAATTCGAAGGAAATTCGAAGAGTCATCTGA 317
QY	679 GGAACCCACATGATCTCCAGGCTTCCAGGCGCGAAGCGGAGAGGAAAGACAGCT 738
DB	318 GGAACCCACATGATCTCCAGGCTTCCAGGCGCGAAGCGGAGAGGAAAGACAGCT 377
QY	739 CAGGACCCAGTGTGAGGCTTACAAGCAGAGAGGAGACCTGTGGGCATCGTCTGA 798
DB	378 CAGGACCCAGTGTGAGGCTTACAAGCAGAGAGGAGACCTGTGGGCATCGTCTGA 437
QY	799 ACTGCAGCTCAAGCTCAACTCCAGCGCTCCTCAGAGATTTCCTTTGTGAAATTAGGAT 858
DB	438 ACTGCAGCTCAAGCTCAACTCCAGCGCTCCTCAGAGATTTCCTTTGTTGAAATTAGGAT 497
QY	859 GGTGAAGGAGAGCAGAGGGTCAGTAAAGAAATCAAGCATAGTCTGGGCCACGAG 918
DB	498 GGTGAAGGAGAGCAGAGGGTCAGTAAAGAAATCAAGCATAGTCTGGGCCACGAG 557
QY	919 AACAGTCTCCACTGGCACGGCATTTGCTAAATATAGGAGCAGATCTGCAGATGGGCCAA 978
DB	558 AACAGTCTCCACTGGCAC-----GAGCAGATCTGCAGATGGGCCAA 599
QY	979 GAATTACTTCGAACATGAGGAGTTAACTGTGAGCAGCTCCTGTGCTCCCTAAAGGGAAG 1038
DB	600 GAATTACTTCGAACATGAGGAGTTAACTGTGAGCAGCTCCTGTGCTCCCTAAGGGAAG 659
QY	1039 GAATCAGAAGTGGAGAGACTTGAAGTTGCATCAAGGAGGCCAAAGAAAGATTTCAGA 1098
DB	660 GAATCAGAAGTGGAGAGACTTGAAGTTGCATCAAGGAGGCCAAAGAAAGATTTCAGA 719
QY	1099 TTTTGAAGAAAGAAACAGATTAATCGTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAG 1158
DB	720 TTTTGAAGAAAGAAACAGATTAATCGTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAG 779
QY	1159 GAAAGAGAAATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGAAGCACTGAA 1218
DB	780 GAAAGAGAAATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGAAGCACTGAA 839
QY	1219 CCTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC 1278

DB	840	CCTCAGGTGACATCTCTGTTTAAGAGGCTTCAAGAGGCTCATACAAAACCTCAGCGAGC	899
QY	1279	TGAGCTAATGAAGAAGAGACTTTCAAGAAAGTGTGAGGCCCTTGAAGAGAAAATTTCTGC	1338
DB	900	TGAGCTAATGAAGAAGAGACTTTCAAGAAAGTGTGAGGCCCTTGAAGAGAAAATTTCTGC	959
QY	1339	AATTCATCAGAGTTGAATGAAGAAAGCAGAGCTTGTATTACTATAACAAAAGTTAGAGCT	1398
DB	960	AATTCATCAGAGTTGAATGAAGAAAGCAGAGCTTGTATTACTATAACAAAAGTTAGAGCT	1019
QY	1399	ACAAGTGAAGAGCATGCTATCAGAATCAAAATGGAACAGGCTTAAACACAGAGATCAAAA	1458
DB	1020	ACAAGTGAAGAGCATGCTATCAGAATCAAAATGGAACAGGCTTAAACACAGAGATCAAAA	1079
QY	1459	GTCCAAATTAACCTGTGCTACAGATGACACACAACAGCTTCTTCAAGAACATTAATATGC	1518
DB	1080	GTCCAAATTAACCTGTGCTACAGATGACACACAACAGCTTCTTCAAGAACATTAATATGC	1139
QY	1519	ATTGAAAAACAATTGAGGAATACTAACAAAGAAAGTGCAGAAAAAGTGCAGGCGAGTCT	1578
DB	1140	ATTGAAAAACAATTGAGGAATACTAACAAAGAAAGTGCAGAAAAAGTGCAGGCGAGTCT	1199
QY	1579	GAGGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAAACAGCTGCA	1638
DB	1200	GAGGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAAACAGCTGCA	1259
QY	1639	AATGATGAATTAAGCAACCAATTCGCAAGCAGGAGAGGACCTGGAAACCAATGACCAT	1698
DB	1260	AATGATGAATTAAGCAACCAATTCGCAAGCAGGAGAGGACCTGGAAACCAATGACCAT	1319
QY	1699	CCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTGCTGAAAGAGCAGGAGAGA	1758
DB	1320	CCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTGCTGAAAGAGCAGGAGAGA	1379
QY	1759	GAAATTCATGAGGAAAGAGCAACTGGCATTGTCAGCTGGCAGTCTGCTGAAAGAGAA	1818
DB	1380	GAAATTCATGAGGAAAGAGCAACTGGCATTGTCAGCTGGCAGTCTGCTGAAAGAGAA	1439
QY	1819	TGATGCTTTGAAAGCAGGAGGAGGAGTCTTGTGATGAGATCAGAGTCTCATGGGGC	1878
DB	1440	TGATGCTTTGAAAGCAGGAGGAGGAGTCTTGTGATGAGATCAGAGTCTCATGGGGC	1499
QY	1879	GAGAACAGTGAATCTGACAGCAGGCTTACCTTGTTCAGAGAGGAGCTCAGGACAGGA	1938
DB	1500	GAGAACAGTGAATCTGACAGCAGGCTTACCTTGTTCAGAGAGGAGCTCAGGACAGGA	1559
QY	1939	CTGGCGGCAACAGCGGAATATTCCGATTTCCTGCCCCAAGTGTGGAGAGGTTCTGCCC	1998
DB	1560	CTGGCGGCAACAGCGGAATATTCCGATTTCCTGCCCCAAGTGTGGAGAGGTTCTGCCC	1619
QY	1999	TGACATAGACACGTTTACAGATTCACGTCGATGGAATTCATCATTTAAGTGTGATGATCA	2058
DB	1620	TGACATAGACACGTTTACAGATTCACGTCGATGGAATTCATCATTTAAGTGTGATGATCA	1679
QY	2059	CCTCCCCAAAACCTGTTGGT 2077	
DB	1680	CCTCCCCAAAACCTGTTGGT 1698	
RESULT 25			
AD043193			
ID AD043193 standard; cDNA; 1925 BP.			
XX			
AC AD043193;			
XX			
DT 29-JUL-2004 (first entry)			
XX			
DE Macaque optineurin cDNA.			
XX			
KW Mouse; optineurin; glaucoma; diagnosis; gene therapy; ophthalmological;			
KW gene; ss.			
XX			

OS Macaca mulatta.  
 FH Key Location/Qualifiers  
 FT CDS 90..1805  
 FT /\*tag= a  
 FT /product= "Macaque optineurin"  
 PN WO2004039312-A2.  
 XX  
 PD 13-MAY-2004.  
 XX  
 PF 26-JUN-2003; 2003WO-US020165.  
 XX  
 PR 25-OCT-2002; 2002US-00281457.  
 XX  
 PA (UYCO-) UNIV CONNECTICUT.  
 PA (SGEO-) ST GEORGES ENTERPRISES LTD.  
 XX  
 PI Sarfarazi M, Rezaie T, Child AH;  
 XX  
 DR WPI; 2004-376046/35.  
 DR P-PSDB; ADO43194.  
 XX  
 PT New optineurin nucleic acids and polypeptides having sequence  
 PT alterations, which indicates the presence of an optineurin-associated  
 PT (risk of) glaucoma, useful for detecting or diagnosing glaucoma, e.g.  
 PT primary open angle glaucoma.  
 XX  
 PS Example; SEQ ID NO 11; 110pp; English.  
 XX  
 CC The present sequence is that of macaque optineurin (optic neuropathy  
 CC inducing protein) cDNA. Comparison of protein sequences, and Western  
 CC blotting results, indicate conservation of optineurin as shown in human  
 CC ADO43184, macaque, mouse, rat, pig and cattle sequences. Overall, human  
 CC optineurin has 78-85% sequence identity with its homologues in mouse,  
 CC rat, pig and cattle, and 96% identity with macaque. Mutation of the human  
 CC optineurin gene is associated with primary open angle glaucoma. 2  
 CC Mutations, E50K and M98K, found in human optineurin are also found in  
 CC macaque, corroborating evidence that this mutation is a risk factor for  
 CC glaucoma. The E50K mutation is further conserved in mouse and bovine.  
 CC Methods of detection, prognosis and diagnosis of the presence or absence  
 CC of optineurin-associated glaucoma or of an optineurin-associated  
 CC increased risk of glaucoma are described, in which a sample is tested for  
 CC the presence of certain gene sequence alterations or for alterations in  
 CC the expression or activity of the optineurin protein. Also described are  
 CC methods of therapy of glaucoma, including gene therapy methods.  
 XX  
 SQ Sequence 1925 BP; 632 A; 403 C; 518 G; 372 T; 0 U; 0 Other;  
 Query Match 78.4%; Score 1629.4; DB 12; Length 1925;  
 Best Local Similarity 95.3%; Pred. No. 0;  
 Matches 1697; Conservative 0; Mismatches 66; Indels 18; Gaps 1;  
 QY 297 CAGGAACCTCTGCAATGTCCTCCATCAACCTCTCAGCTGCCTCCTGAAAGGAGGACAGCC 356  
 DB 76 CAGGAACCTCTGCAATGTCCTCCATCAACCTCTCAGCTGCCTCCTGAAAGGAGGACAGCC 135  
 QY 357 CCAGTGAAGCAGAGGAATGGACCCGCCACCTGGCCACCCAAACCTGGACACGTTTA 416  
 DB 136 CCAGTGAAGCAGAGGAATGGACCCGCCACCTGGCCACCCAAACCTGGACACATTC 195  
 QY 417 CCCCGAGGAGCTGCTCAGCAGATGAAAGAGCTCTTGACCAAGAACCCAGCTGAAAG 476  
 DB 196 CCCCGAGGAGCTGCTCAGCAGATGAAAGAGCTCTTGACCGGAAACCCAGCTGAAAG 255  
 QY 477 AAGCCATGAGCTTAATAATCAAGCCATGAAGGAGATTGAGGAGCTTTCGCGCTGGA 536  
 DB 256 AAGCCATGAGCTTAATAATCAAGCCATGAAGGAGCTTTCGCGCTGGA 315  
 QY 537 CAGAGAAACAGAGGAAGACCGCAGTTTTTTTGAGATACAGAGCAAGAGCAAGAGAGC 596  
 DB 316 CAGAGAAACAGAGGAAGACCGCAGTTTTTTTGAGATACAGAGCAAGAGCAAGAGAGC 375

QY 597 GTCTAATGSCCTTGAGTCAATGAGAAATGAGAAAGAGCTTGAGAAATCTAAAG 656  
 DB GTCTCATGSCCTTGAGTCAACGAGAAATGAGAAATGAGAAAGAGCTTGAGAAATCTAAAG 435  
 QY 657 GGAATCAGAAAGGTCTGAGGACCCCACTGATGACTCCAGGGTCCCGAGGCGCAG 716  
 DB 436 GGAATCAGAAAGGTCTGAGGACCCCACTGATGACTCCAGGGTCCCGAGGCGCAG 495  
 QY 717 CGGAGCAGGAAAGGACCCAGCTCAGGACCCAGGTGCTGAGGCTACAACGACAGAGGAG 776  
 DB 496 CGGAGCAGGAAAGGACCCAGCTCAGGACCCAGGTGACGAGGCTACACGAGAGAGGAG 555  
 QY 777 ACCTGTTGGGCATCGTGTCTGAACTGACGCTCAAGCTGAACTCCAGCGGCTCTCTCAG 836  
 DB 556 ACCTGTTGGGCATCGTGTCTGAACTGACGCTCAAACTGAACTCCAGCGGCTCTCTCAG 615  
 QY 837 ATTCCTTTGTTGAAATTAGGATGCTGAGGAGAGCAGAGGAGGTCAGTAAAGAAATCA 896  
 DB 616 ACTCCTTTGTTGAAATTAGGATGCTGAGGAGAGCAGAGGAGGTCAGTAAAGAAATCA 675  
 QY 897 AGCATAGTCTCTGGGCCCAACGAGAAACAGTCTCCACTGGCCAGCGCATTTGCTAAATATAG 956  
 DB 676 AGCATAGTCTCTGGGCCCAACGAGAAACAGTCTCTCATTTGGCAC-----GA 717  
 QY 957 GCAGATCTGACAGATGGGGCCCAAGAAATTACTTCGAACATGAGAGGAGTAACTGTGAGCC 1016  
 DB 718 GCAGATCTGACAGAGGGGCCCAAGAAATTACTTTGGAACATGAGGAGTAACTGTGAGCC 777  
 QY 1017 TCCTGCTGTGCTTAAGGAGGAGGAAATCAGAAAGTGGAGAGACTTGAAGTTCGACTCAAGG 1076  
 DB 778 TCCTGCTGTGCTTAAGGAGGAGGAAATCAGAAAGTGGAGAGACTTGAAGTTCGACTCAAGG 837  
 QY 1077 AGGCCAAAGAAAGATTTTCAGATTTTCAAAAGAAACCAAGTAATCGTCTCAGAGTTGAAA 1136  
 DB 838 AGGCCAAAGAAAGATTTTCAGATTTTCAAAAGAAACCAAGTAATCGTCTCAGAGTTGAAA 897  
 QY 1137 CCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGAGAGCTGTGTG 1196  
 DB 898 CCCAGACAGAGGGGAGCAGAGAAAGAGAAACGAGAGAGAGAAAGGCCCGAGAGCTGTGTG 957  
 QY 1197 GAAGCGAAGTGAAGCACTGAACTCCTCAGGTGACATCTGTGTTAAGGAGCTTCAAGAGG 1256  
 DB 958 GAAGCGAAGTGAAGCACTTGAACCTTCAGGTGACATCTGTGTTAAGGAGCTTCAAGAGG 1017  
 QY 1257 CTATACAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGTGAGG 1316  
 DB 1018 CTATACAAACCTCAGTGAAGCCGAGCTAATGAAGAGAGACTTCAAGAAAGTGTGAGG 1077  
 QY 1317 CCCTTGAAGGAGGAGGAAATTTCTGCAATTCATCAGAGTTGAAATGAAAGCAAGAGCTTGT 1376  
 DB 1078 CCCTTGAAGGAGGAGGAAATTTCTGCAACTCCATCAGAGTTGAATGAAAGCAAGAGCTTGT 1137  
 QY 1377 ATACTAAGGAGGTTAGAGCTACAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAC 1436  
 DB 1138 ATACTAAGGAGGTTAGAGCTACAGTGAAGAGCATGCTCTCGGAAATCAAAATGGAAC 1197  
 QY 1437 AGGCTAAACAGAGGAGTGAAGCTCCAAATTTAATCTGCTACAGATGACACACAAAGC 1496  
 DB 1198 AGGCTAAACAGAGGAGTGAAGCTCCAAATTTAATCTGCTACAGATGACACACAAAGC 1257  
 QY 1497 TTCTTCAAGAACATAATAATGCAATTTGAAACAAATTTGAGGAACTAAACAGAAAGAGT 1556  
 DB 1258 TTCTTCAAGAACATAATAATGCAATTTGAAACAAATTTGAGGAGCTTAAAGAGAGT 1317  
 QY 1557 AAAAGTGGACAGGCGAGTGTCTGAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAGG 1616  
 DB 1318 AAAAGTGGACAGGCGAGTGTCTAAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAGG 1377  
 QY 1617 CTCTGCTTCCAAACAGCTGCAATGGAATGAGCAAACTGGAATGCGCAGAGAGG 1676  
 DB 1378 CTCTGCTTCCAAACAGCTGCAATGGAATGAGCAAACTGGAATGCGCAGAGAGG 1437  
 QY 1677 AGGACCTGGAAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTC 1736

|||||  
1438 AGGACCTGGAACCATGACCGTCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTC 1497  
QY 1737 ATGCTGAAGAGCAGGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCATTGCAGC 1796  
Db 1498 ATGCTGAAGAGCAGGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCATTGCAGC 1557  
QY 1797 TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGGAGGAGCGAGTCCTTGATGG 1856  
Db 1558 TGGCAGTTTCTGTAAGAGAAATGATGCTTTTGAAGATGGAGGAGCGAGTCCTTGATGG 1617  
QY 1857 AGATGAGAGTCTGATGGGCGAGAACAGTACTCTGACAGGAGGCTTACCTTGTTTC 1916  
Db 1618 AGATGAGAGTCTGATGGGCGAGAACAGTACTCTGACAGGAGGCTTACCTTGTTTC 1677  
QY 1917 AAAGAGGAGTGAAGGAGGAGTGGCGGCAACAGCGGAATATTCGATTTCCTGCTGCC 1976  
Db 1678 AAAGAGGAGTGAAGGAGGAGTGGCGGCAACAGCGGAATATTCGATTTCCTGCTGCC 1737  
QY 1977 CCAAGTGTGAGAGGTTCTGCTTGACATGACACGTTTACAGATTTCAGTGATGGATTGCA 2036  
Db 1738 CCAAGTGTGAGAGGTTCTGCTTGACATGACACGTTTACAGATTTCAGTGATGGATTGCA 1797  
QY 2037 TCATTTAAGTGTGATGATATCACTCCCAAAACTGTTGGT 2077  
Db 1798 TCATTTAAGTGTGATGATGATCACTCCCAAAACTGTTGGT 1838

RESULT 26  
ADO43199  
ID ADO43199 standard; cdna; 1799 BP.  
XX ADO43199;  
AC  
XX  
XX  
XX 29-JUL-2004 (first entry)  
XX  
XX Pig optineurin cdna.  
DE  
XX  
XX Pig; optineurin; glaucoma; diagnosis; gene therapy; ophthalmological;  
KW gene; ss.  
XX  
XX Sus scrofa.  
FH Key Location/Qualifiers  
FT 1.1725  
FT CDS /\*tag= a  
XX  
XX WO2004039312-A2.  
XX  
XX 13-MAY-2004.  
XX  
XX 26-JUN-2003; 2003WO-US020165.  
XX  
XX 25-OCT-2002; 2002US-00281457.  
XX  
XX (UYCO-) UNIV CONNECTICUT.  
XX (SSEO-) ST GEORGES ENTERPRISES LTD.  
XX  
XX Sarfarazi M, Rezaie T, Child AH;  
XX  
XX WPI; 2004-376046/35.  
XX P-PSDB; ADO43200.  
XX  
XX New optineurin nucleic acids and polypeptides having sequence  
PT alterations, which indicates the presence of an optineurin-associated  
PT (risk of) glaucoma, useful for detecting or diagnosing glaucoma, e.g.  
PT primary open angle glaucoma.  
XX  
XX Example; SEQ ID NO 17; 110pp; English.  
XX  
XX The present sequence is that of pig optineurin (optic neuropathy inducing  
CC protein) cdna. Comparison of protein sequences, and Western blotting  
CC results, indicate conservation of optineurin as shown in human ADO43184,  
CC

macaque, mouse, rat, pig and cattle sequences. Overall, human optineurin  
CC has 78-85% sequence identity with its homologues in mouse, rat, pig and  
CC cattle, and 96% identity with macaque. Mutation of the human optineurin  
CC gene is associated with primary open angle glaucoma. 2 Mutations, E50K  
CC and M98K, found in human optineurin are also found in macaque,  
CC corroborating evidence that this mutation is a risk factor for glaucoma.  
CC The E50K mutation is further conserved in mouse and bovine. Methods of  
CC detection, prognosis and diagnosis of the presence or absence of  
CC optineurin-associated glaucoma or of an optineurin-associated increased  
CC risk of glaucoma are described, in which a sample is tested for the  
CC presence of certain gene sequence alterations or for alterations in the  
CC expression or activity of the optineurin protein. Also described are  
CC methods of therapy of glaucoma, including gene therapy methods.  
XX  
SQ Sequence 1799 BP; 636 A; 366 C; 454 G; 343 T; 0 U; 0 Other;  
Query Match 62.2%; Score 1291; DB 12; Length 1799;  
Best Local Similarity 84.6%; Pred. No. 0;  
Matches 1495; Conservative 0; Mismatches 245; Indels 27; Gaps 3;  
QY 311 ATGTCCCATCAACCTCTCAGCTGCTCACTGAAAAGAGGAGCAGCCCGTAGTAAAGCACA 370  
Db 1 ATGTCCCATCAACCTCTGAGCTGCTGACTGAGAGGGGGACAGCCCGAAACCCACA 60  
QY 371 GGAATGGAACCCCGCCACCTGGCCCGACCCAAACCTTGACACGTTTACCCCGGAGGAGCTG 430  
Db 61 GGAATGGAACCCCGCCACCTGGCTTACCCAAACCTTGACACGTTTACCCCGACATGAACTG 120  
QY 431 CTGACGACGATGAAGAGAGCTCTCTGACCAAGAACCCACGCTGAAAAGACCATGAAGCTA 490  
Db 121 CTGACGACGATGAGAGAGCTTCTATCGAGAACCATCAGCTGAAAGAGCCATGAAGCTA 180  
QY 491 AATAATCAAGCCATGAAGGGAGATTGTAGGAGCTTTCGGCCTTGGACAGAGAACAGAG 550  
Db 181 AATAATCAAGCTATGAAGGGCGATTGTAGGAGCTTTCAGCCTTGGACAGAGAACAGAG 240  
QY 551 GAAGAACGCGAGTTTTTTCAGATACAGAGCAAGAGCAAGAGCGTCTTAATGGCGCTTG 610  
Db 241 GAAGAACGCGCTTTTTTTCAGACCCAGAGCAAGAGCGCCAAAGAGCGCTTAAACGGCTCTG 300  
QY 611 AGTCATGAGAAATGAGAAATTTGAAGAGAGCTTGGAAAACTAAAGGGAAATCAGAAAGG 670  
Db 301 AGTCCTGAATGAAATGAAATCTGAAGCAAGAACTTGGAAACTAAAGGGAAATCAGAAAGG 360  
QY 671 TCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCCGAGCGGAGCAGGAAAAG 730  
Db 361 TCATTTGAGACCTCACTGGGGACCCCGAGGGTCCCAAGCGGAGCAGAACAGGAGTA 420  
QY 731 GACGAGCTCAGGACCCAGGTGGTGGCTACAGCAGAGAGGAGCAGACCTGTTGGGCATC 790  
Db 421 GAAACAGCTGAAGACCCAGGTGGCAGCGCTTCAAGCTGAAAAGCGGATCTGCTGGGCATC 480  
QY 791 GTGTCTGAAGCTCAGCTCAAGCTGAACTCCAGCGGCTCTCTCAGAAGATTCCTTTGTTGAA 850  
Db 481 GTGTCTGAATTCAGCTCAAGCTGAAGTGGGCGCTCTCTGAGACTCTCTTTGTTGAA 540  
QY 851 ATTAGGATGCTGAAGGAGAGCAGAGGCTCAGTAAAGAAATCAAGCATATGCTCTGGG 910  
Db 541 ATCAGGATGCTGAGGAGAGCAGATGACAGCAATGAAGGAAATCAAGACAAAGTCCTGGG 600  
QY 911 CCCACGAGAACAGTCTCCACTGGCAGCGCATTTCTTAAATATAGGAGCAGATCTGCAGAT 970  
Db 601 CCCATAAGAACTGATTCCTTGCAC-----GACAAATCTGCAGAA 642  
QY 971 GGGGCCAAGAAATTAATTCGAAATGAGAGCTTAATCTGAGCCAGCTCTCTGCTGTGCTA 1030  
Db 643 GGTACCAAGAAATTAATTCGAAATTAATCTGAGCCAGCTCTCTGCTGTGCTA 702  
QY 1031 AGGGAAGGGAATCAGAGGTTGAGAGACTTGAAGTTGCACTCAAGGAGGCCAAGAAAGA 1090  
Db 703 AGGGAAGGAAACAGAGAGGTTGAGAGACTTGAATTCGCTCAAGGAGGCCAAGAAAGA 762  
QY 1091 GTTTCAGATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGG 1150



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Db 763 ATTTAGATTTTGAAGAAGAAACCCAGGATCGTTCTGAGACTGAGACCCAGACAGAG 822
Qy 1151 AGCAGAGAAAGAAATCATGAAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGGAA 1210
Db 823 CACAAAGAACAGAGAAAGAGAGAGAAAGCCAGAAACTGTTGGAAGTGAAGTGGAA 882
Qy 1211 GCAGTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGTTCAGAGGCTCATACAAACTC 1270
Db 883 ATGTTAAACCTTCAGGTGACACCTGTTTAAAGGAGTTCAGAGGCTCAGACGAACTC 942
Qy 1271 AGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTCAAGCCCTTGAAGGAAA 1330
Db 943 AGTGAAGCTGAGCTCATGAAGAGAGACTTCAAGAAAATGTCAAGCACTTGAAGGAAA 1002
Qy 1331 AATTCTGCAATTCATCAGAGTTGAATGAAAAGCAAGAGCTGTTTATATACTAAACAAAAG 1390
Db 1003 AATTCTGCAACCCCATCAGACTGAATGAAGAAGCAAGAGCTTCTTTATATAACAAAAG 1062
Qy 1391 TTAGAGCTACAAGTGGAAAGCATGTCTATCAGAAATCAAAATGGAAAGCTTAAACAGAG 1450
Db 1063 TTGAGCTCCAAAGTGGAAAGCATGAGATCAGAAATTTAAATGGAGCAAGCCAAAACAG 1122
Qy 1451 GATGAAGAGTCCAAATTAACCTGTCTACAGATGACACACAAGCTTCTTCAAGACAT 1510
Db 1123 GAGGAAAAGTCCAAATTAACCTGTCTACAGTTGACCCACACAGGCTTCTTCAAGATAC 1182
Qy 1511 AATAATGCATTTGAAAACAAATTAAGGAACCTAAACAGAAAGAGTCAAGAAAAGTGACAGG 1570
Db 1183 AATAATGCACCTGAAAACAAATTAAGGAACCTGAAAAGAGAGAGTCTGAAAAGTGGATAG 1242
Qy 1571 GCAGTGTGAAGAACTAGTGAAGAACTGGAACCTGGCAGAGAGAGGCTCTGGCTTCCAAA 1630
Db 1243 GTGGTGTCTGAGGAACCTGAATGGAAAGCTGGAATGGCAGAGAGGCTTGGCTTCCAG 1302
Qy 1631 CAGTGCNAATGGATGAATCAAGCAACCATTTGCCAAGCAGGAGAGGAGCTGGAAC 1690
Db 1303 CAGTCCAAATGGATGAATGAAGCAGACCACTTGCACAGCAGAGAGGAGCTGGAAC 1362
Qy 1691 ATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGCTGAAGAGCA 1750
Db 1363 ATGGCTGTTCTCAGGGCTCAGATGAGGTATACCTGTTCTGACTTTCATGCTGAAGAGCA 1422
Qy 1751 GCGAGAGAGAAATTCATGAGGAAAAGGAGCAACTGGCAATTCAGCTGGCAGTTCCTGCTG 1810
Db 1423 GCAAGAGAGAGATTCATGAAGAAAGAGGCAACTGGCAATTCAGCTGGCAGTTCCTGCTG 1482
Qy 1811 AAAGAGATGATGCTTTTGAAGAGCGAG---GCAAGCAGTCCCTTGAATGGAGATCAGAGT 1867
Db 1483 AAAGCAGCAATGCTTTTGAAGAGGAGCCAGCAGGCAATCCTTGAATGGAGATCAGAGC 1542
Qy 1868 CGTCATGGGCGAGAACAGTGAATCTGACAGCAGGCTTACCTTGTTCAGAGAGGAGCT 1927
Db 1543 CGTCATGGGCGAGAACAGTGAATCTGACAGCAGGCTTTCCTTGTTCAGAGAGGAGCT 1602
Qy 1928 GAGCAGGAGGAGTGGCGCAACAG-----CGGAATATTCGATTCATTCCTGCCCCAAG 1981
Db 1603 GAGGATAGAACTGGCTGCAACACACACAGAAATTTCAATTCATTCCTGCCCCAAG 1662
Qy 1982 TGTGGAGAGGTTTGTGCTGACATAGACAGTTTACAGATTCACGTGATGGATTCGATCATT 2041
Db 1663 TGTGGAGAGGTTTGTGCTGACATAGATACACTACTGATTCACGTTCACGAGTGCATCATT 1722
Qy 2042 TAAAGTGTGATGATACCTCCCCAAA 2068
Db 1723 TAAAGTGTGATTTTACTTCCCCAAA 1749
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RESULT 27  
ADO43191  
ID ADO43191 standard; cDNA; 2023 BP.  
XX  
AC ADO43191;

```
XX DT 29-JUL-2004 (first entry)
XX DE Mouse optineurin cDNA.
XX KW Mouse; optineurin; glaucoma; diagnosis; gene therapy; ophthalmological;
XX KW gene; ss.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT CDS 151..1905
XX FT /*tag= a
XX FT /product= "Mouse optineurin"
XX WO2004039312-A2.
XX PN 13-MAY-2004.
XX PD 26-JUN-2003; 2003WO-US020165.
XX PF 25-OCT-2002; 2002US-00281457.
XX PR (UYCO-) UNIV CONNECTICUT.
XX PA (SGEO-) ST GEORGES ENTERPRISES LTD.
XX FA Sarfarazi M, Rezaie T, Child AH;
XX DR WPI; 2004-376046/35.
XX DR P-ESDB; ADO43192.
XX PT New optineurin nucleic acids and polypeptides having sequence
XX PT alterations, which indicates the presence of an optineurin-associated
XX PT (risk of) glaucoma, useful for detecting or diagnosing glaucoma, e.g.
XX PT primary open angle glaucoma.
XX PS Example; SEQ ID NO 9; 110pp; English.
XX CC The present sequence is that of mouse optineurin (optic neuropathy
XX CC inducing protein) cDNA. It encodes a 584-amino acid proteins that shows
XX CC 78% identity to human optineurin ADO43184. Comparison of protein
XX CC sequences, and Western blotting results, indicate conservation of
XX CC optineurin as shown in human, macaque, mouse, rat, pig and cattle
XX CC sequences. Overall, human optineurin has 78-85% sequence identity with
XX CC its homologues in mouse, rat, pig and cattle, and 96% identity with
XX CC macaque. Mutation of the human optineurin gene is associated with primary
XX CC open angle glaucoma. 2 Mutations, E50K and M98K, found in human
XX CC optineurin are also found in macaque, corroborating evidence that this
XX CC mutation is a risk factor for glaucoma. The E50K mutation is further
XX CC conserved in mouse and bovine. Methods of detection, prognosis and
XX CC diagnosis of the presence or absence of optineurin-associated glaucoma or
XX CC of an optineurin-associated increased risk of glaucoma are described, in
XX CC which a sample is tested for the presence of certain gene sequence
XX CC alterations or for alterations in the expression or activity of the
XX CC optineurin protein. Also described are methods of therapy of glaucoma,
XX CC including gene therapy methods.
SQ Sequence 2023 BP; 614 A; 473 C; 578 G; 358 T; 0 U; 0 Other;
```

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Query Match 53.0%; Score 1101.8; DB 12; Length 2023;
Best Local Similarity 77.5%; Pred. No. 2.4e-288;
Matches 1439; Conservative 0; Mismatches 352; Indels 66; Gaps 6;

Qy 263 GAGAAAGTGGCAACTTTTGGAGTGACTTTTCCACAGGAACCTTCTGCAATGTCCCCATCAA 322
Db 103 GAAGCAGTGACCTAAGAGGAGAGGATCCCTGTGCGCGACCTGTTCACATGTCCCCATCAA 162
Qy 323 CCTCTCAGCTGCTCACTGAAAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 382
Db 163 CCTCTCAGCTGCTCACTGAAAAGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 222
Qy 383 CCCCACTGGCCCAACCAACCTGGACACGTTTACCCCGAGGAGCTGCTGCGAGCAGATG 442
```

Dbb 223 TCCAAATATGTTTCACCCCAGCCCTGGACACATTCACCCCTGAGGAGCTGCTGCAGCAATG 282  
Qy 443 AAAGAGATCTCTGACCAAGAACCCAGCTGAAAGAGCCATGAGCTAAATATCAAGCC 502  
Dbb 283 AAGGAACTCTGTTGAGAACCCAGCTGAAAGAGCCATGAGCTAAATATCAAGCT 342  
Qy 503 ATGAAAGGAGATTTGAGGAGCTTTGCGCTGACACAGAGAAACAGAGGAGAACCCAG 562  
Dbb 343 ATGAAAGGCGATTTGAGGAGCTGTCGCGCTGACACAGAGAGAGAGAGAGCGCCTG 402  
Qy 563 TTTTGTGAGATACAGAGCAAGAGCAAAAGAGCGTCTAATGCGCTTGGTCAATGAGAAT 622  
Dbb 403 TTTGTTGAGATGCAAGCAAGAGAGTTAAGAGCGCTTAAAGCCCTGACTCATGAGAAAT 462  
Qy 623 GAGAAATTTGAGGAAGCTTTGAAAACTAAAGGGGAAATCAGAAAGGTCATCTGAGGAC 682  
Dbb 463 GAGAGGCTGAAGGAAGCTTTGAAAAATTCAGAGAGAAATCAGAAAGCCATTTGGAAGAC 522  
Qy 683 CCCACTGATGATCCAGGCTTCCAG-----GGCC 712  
Dbb 523 CTCACAGGTGGCTACAGGTATCCAGAGCCCTTGGAGGAGGAAGTGGAGAGCTGGAAGACC 582  
Qy 713 GAAGCGGAGCAGAAAGAGGACAGCTCAGGACCCAGGTGCTGAGGCTTACAGCAGAGAG 772  
Dbb 583 CAGGTGAGCAGGAGAGTGGAGCATCTGAAGATCAGGTGATGCGCTTCGGGCTGAAAG 642  
Qy 773 GCAGACCTGTTGGGCATCGTGTCTGAACCTCAGCTCAGCTGAACTCCAGCGCTCCTCA 832  
Dbb 643 GCAGACCTGTTGGGCATCGTCTCAGAACTGCAGCTCAAACTCAACTCCGCGGCTCCTCG 702  
Qy 833 GAGATTCCTTTGTTGAAATAGATGGCTGAAGGAGAGACAGAGGTCAGTAAAGAA 892  
Dbb 703 GAAGACTCTCTCGTTGAGATCAGATGACCGAAGGAGAGACTGAAGGGGCAATGGAAGGAG 762  
Qy 893 ATCAGCATAGTCTCGGGCCACAGAGAACTCTCCACTGCGCAGGCAATGTTCTAAATAT 952  
Dbb 763 ATGAAGAACTGCCCCATACCCCAAGAAACAGACCCCATCAGC----- 804  
Qy 953 AGGACGAGATCTGCAGATGGGGCCCAAGAAATTACTTCGAAATGAGGAGTTAACTGTGAGC 1012  
Dbb 805 TTGAGCAACTGTACAGAGGATGCCAGGAGTTGTCCGAGTTTGAAGAACTGACTGTGAGC 864  
Qy 1013 CAGCTCTGCTGTGCTTAAGGGAAGGAATCAGAGGTGAGAGACTTGAAGTTGACATC 1072  
Dbb 865 CAGCTTCTGCTTGGCTTAAGGGAAGGAACCAAAAGGTGAGAGACTTGAAGTCGCCCC 924  
Qy 1073 AAGGAGCCAAAGAAAGATTTCAAGATTTTGAAGAAAGAAACAAAGTAACTCGTTCTGAGATT 1132  
Dbb 925 AGAAGCCCAAGAAAGAAATTTCAAGATTTTGAAGAAAGAAAGCAATGGCCCAATTTCTTACT 984  
Qy 1133 GAAACCCAGACAGAGGGGAGCAGACAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACT 1192  
Dbb 985 GAGAGCAGACAGCGAGGAGCAGACAGAGAGA---AGGAGCAAGGCCAAGAGAGT 1041  
Qy 1193 GTTGAAGCGAAGTGAAGACCTGAACCTCAGGTGACATCTCTGTTTAAGGAGCTTCAA 1252  
Dbb 1042 GTTGAAGCGAAGTGAAGAACTGAGCAATTCAGTGACCTCTCTGTTTAAGGAGCTTCAA 1101  
Qy 1253 GAGCTCATACAAACTCAGCGAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGT 1312  
Dbb 1102 GAGGCAACACAAAACTCAGTGAGGCTGAGCTGATGAAGAGAGACTTCAAGAAAGTGT 1161  
Qy 1313 CAGGCCCTTGAAGGAAAAATTTGCAATTCATCAGAGTTGAATGAAAGCAGAGAGCTT 1372  
Dbb 1162 CAGGCTCTGGAGAGAAAGACTCTGCAACACCATCAGAGCTGAATGAAAGCAGAGGCTC 1221  
Qy 1373 GTTTATTAACAAAAATTTAGAGCTACAGTGAAGAGCATGCTATCAGAAATCAAAATG 1432  
Dbb 1222 GTTTACAGTAACAAAGAGTTAGAGCTGAGGTGAGAGCATGCGCTCCGAAATCAAGATG 1281  
Qy 1433 GAACAGGCTAAACAGAGGATGAAAGTCCCAATTAAGTGTGCTACAGATGACACACAAC 1492  
Dbb 1282 GAGCAGGCCAAGACAGAGGAGGAGAGAGTCCAGGTTAGCCACTCTGTCAGGCAACTCAAC 1341

## RESULT 28

ADP80916  
ID ADP80916 standard; cDNA; 1752 BP.

XX AC ADP80916;

XX AC ADP80916;

DT 09-SEP-2004 (first entry)

XX Mouse optineurin nucleotide sequence SEQ ID NO:141.

XX c-fos; c-fos interacting protein; fos interacting protein chromosome X;  
KW Fip-cx; screening; Fc-fos interacting protein inhibitor; mouse;  
KW optineurin; gene; ss.

XX Mus musculus.

PH Key Location/Qualifiers

FT CDS 1..1752

FT /tag= a

FT /product= "optineurin"

XX WO2004053121-A1.

XX 24-JUN-2004.

XX 19-NOV-2003; 2003WO-JP014749.

XX 11-DEC-2002; 2002JP-00360046.

XX (UYKE-) UNIV KEIO.

[illegible]

	Matches	1396;	Conservative	0;	Mismatches	330;	Indels	71;	Gaps	7;
Qy	297	CAGGAACTTCTGCAATGTCCCATCAACCTCTAGCTGCCTCACTGAAAAGGAGCAGCC	356							
Db	13	CCGGACCTGTTACATGTGCCATCAACCTCTGAGCTGCCTGACTGAAAGGGGGACAGCT	72							
Qy	357	CCAGTCAAAAGCAGAGAAATGGACCCGCCACCTGCGCCACCCAAACCTTGACACAGTTTA	416							
Db	73	CCTGTGAGACCCGAGGAATGGACCTTCAATATGTTTACCCCAACCTTGGACACATTCA	132							
Qy	417	CCCGGAGGAGCTGCTGCAGCAGATGAAAGAGCTCTGACCAAGAAACCAACAGCTGAAAG	476							
Db	133	CTCCTGAGGAGCTGCTGCAGCAATGAAGAACTCTCTGTCGAGAAACCAACAGCTGAAAG	192							
Qy	477	AAGCCATGAAGCTAAATATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGCCCTGGA	536							
Db	193	AAGCCATGAAGCTAAATATCAAGCTATGAAGGGCGATTGAGGAGCTTTCGCCCTGGA	252							
Qy	537	CAGAGAAAACAGAAGGAAGACGCCAGTTTTTCAGATACAGACCAAGAAAGCAAAAGAGC	596							
Db	253	CAGAGGCCAGAGGAAGACGCCAGTTGTTTCAGATACAAAGCAAAAGAGCTTAAGGAGC	312							
Qy	597	GTCTAATGGCCTTGAATCATGAGAAATGAGAAAATTGAAGGAAGAGCTTTGAAAAACTTAAAG	656							
Db	313	GCCTCAAGGCCCTGAGTCATGAAATGAGAGGCTGAGGAAGAGAGCTTGGAAAACTTAAAG	372							
Qy	657	GGAAATCAGAAAGGTATCTGAGGAGCCCACTCATGACTCCAGGCTTCCAGAGGCCG--	713							
Db	373	AGAAATCAGAAAGGCCATTTGAAGACATCACAGTAGATGCGGTTTCCAGAAACCGACT	432							
Qy	714	-----AAGCGAGCAGGAAAAAGGACCAGCTCAGG	742							
Db	433	TGGAGCAGGAAGTGGGAGCAACTGAAGAGCAGCTGGAGCAGGAAGTGGAGCATCTGAAG	492							
Qy	743	ACCCAGTGTGAGGCTTACAAGC---AGAGAAAGCAGACCTGTGTGGCATCGTCTCTGAA	799							
Db	493	ATCCAGTGTAGGCGCCTTCAAGCTTGAGAAAGCGGACCTTGTCTGGGCGATTCTGTCTCAGA	552							
Qy	800	CTGCAGCTCAAGCTGAACCTCCAGCGGCTCCTCAGAGATTCCCTTGTGTGAAATTTAGGATG	859							
Db	553	CTGCAGCTCAAGCTCAACTCCGCGGCTCCTCAGAGACTCCTTCGTGGAGA-CAGGATG	611							
Qy	860	GCTGAAGGAAAGCAGAGGGTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCACAGAGA	919							
Db	612	ACTGAAGGAGAGCGGAAGGGCAATGAAGAGAGATGAGGAACAGCGCTGGACCCACAAAGG	671							
Qy	920	ACAGTCTCCACTGCACGGCATTTGCTTAAATATAGGAGCAGATCTGCAGATGGGCCCAAG	979							
Db	672	ACAGCTCCATCATCTGG-----GCAATGTACAGAGGACGCCAGG	713							
Qy	980	AATTTACTTTCGAAACATGAGGAGTTAACTGTGAGCCAGCTCTCTGCTGTCTCTTAAGGGAAGGG	1039							
Db	714	ACTTGTGTGGATTGTGAGAACTGACTGTGAGCCAACTCTCTGCTTTGCCCTCAGGGAAGGA	773							
Qy	1040	AATCAGAAAGTGTGAGAGACTTGAAGTTGCACTCAAGGAGGCCCAAGAAAGATTTTCAGAT	1099							
Db	774	AACCAAAAGTGTGAGAGACTCGAGATCGCGCTCAGAGAACCCAAAGAAAGAAATTTTCAGAT	833							
Qy	1100	TTTGAAGAAAAACAAGTAATCGTTCTGAGATTGAAACCCACAGACAGAGGGGAGCACAGAG	1159							
Db	834	TTTGAAGAAAGCAACACGCCCATTTCTCGATTGAAACCCACAGACAGAGGGGAGCACAAA	893							
Qy	1160	AAAGAGAAATGATGAAGAAAGGCCCCGGAGACTGTTTGAAGCGGAAGTGAAGCACTGAAC	1219							
Db	894	AAAG---AAGAGGAGGACAAAGACCCAGAGAGTGTGGGAATCGAAGTGGAAACTCTGAAC	950							
Qy	1220	CTCCAGTGCATCTCTGTTTAAAGAGCTTCAAGAGCTCATACAAAACCTCAGCGGAAGCT	1279							
Db	951	GTTCAAGTGGCCTCTCTGTTTAAAGGGCTTCAAGAGCGGCACACAAAGCTCAGTAGGCCC	1010							
Qy	1280	GAGCTAATGAAGAAAGAGACTTCAAGAAAAAGTGTCAAGGCCCTTGAAGAGAAAAATTTCTGCA	1339							
Db	1011	GAGCTGATGAAGAAAGAGACTTCAAGAAAAGTGTCAAGGCTCTGGAAGGAAGAACTCTGCA	1070							





QY 942 TGTCTAAATATAGGAGCAGATCTGCAGATGGGGCCCAAGAAATTACTTCGAACATGAGGAGT 1001  
D 599 -----GAGCAGATCTGCAGATGGGGCCCAAGAAATTACTTCGAACATGAGGAGG 645  
QY 1002 TAACTGTGAGCCAGCTCTCTGCTGCTTAAGGAGGGAATCAGAAAGTGGAGAGACTTG 1061  
D 646 TAACTGTGAGCCAGCTCTCTGCTGCTTAAGGAGGGAATCAGAAAGTGGAGAGACTTG 705  
QY 1062 AAGTTGCACCTCAAGAGGCCCAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAGTAATC 1121  
D 706 AGTTGCTCTC---AGAGGNCACAGAGAGTTTCAGATTTT---GAAAGAAACCAAGNAATC 760  
QY 1122 GTT 1124  
D 761 GTT 763  
RESULT 32  
AD262470  
ID AD262470 standard; DNA; 1200 BP.  
XX AC AD262470;  
XX 30-JUN-2005 (first entry)  
XX DE Murine Optn gene, SEQ ID 2194.  
XX KW Drug screening; Peroxisome Proliferator-Activated Receptor alpha;  
XX KW PAR alpha; gene; ds.  
XX OS Mus musculus.  
XX US US2005084872-A1.  
XX PD 21-APR-2005.  
XX 23-JAN-2004; 2004US-00764420.  
XX 24-JAN-2003; 2003US-0442797P.  
XX 30-MAY-2003; 2003US-0474413P.  
XX (LUMP//) LUM P Y.  
XX (TANY//) TAN Y.  
XX (DAIH//) DAI H.  
XX (MUIS//) MUISE E S.  
XX (BERG//) BERGER J P.  
XX (THOM//) THOMPSON J R.  
Lum PY, Tan Y, Dai H, Muise ES, Berger JP, Thompson JR;  
WPI; 2005-313963/32.  
DDBJ; AK015354.  
Determining whether agent has defined biological activity, by making  
comparison e.g. comparing efficacy value, toxicity value and classifier  
value of agent to reference values, and using results to determine  
whether agent has activity.  
Example 4; SEQ ID NO 2194; Sipp; English.  
The present invention relates to a methods for screening biologically  
active agents, such as candidate drugs, to determine whether the agent  
possesses a defined biological activity. The methods involve making one  
or more comparisons chosen from comparing efficacy value of agent to  
reference efficacy value, comparing a toxicity value of the agent to  
reference toxicity value, comparing a classifier value of the agent to  
reference classifier value, and using the comparison result(s) to  
determine whether the agent possesses the defined biological activity.  
Also claimed is a population of oligonucleotide probes (i) specific for  
measuring the expression levels of members of a classifier population of  
genes or a toxicity-related population of genes. (i) are useful for  
measuring the expression levels of genes that are useful for identifying

agonists or partial agonists of Peroxisome Proliferator-Activated  
Receptor (PPAR) gamma. AD263072-AD263959 are oligonucleotide probes which  
are useful in the method of the invention to measure the expression  
pattern of mouse genes AD262273-AD263071 that yield an expression pattern  
that correlates with the stimulation of PPARalpha receptors by an agent.  
Note: The sequence data for this patent did not form part of the printed  
specification, but was obtained in electronic format directly from USPTO  
at seqdata.uspto.gov/sequence.html?docID=20050084872.  
XX  
SQ Sequence 1200 BP; 373 A; 277 C; 311 G; 239 T; 0 U; 0 Other;  
Query Match 30.2%; Score 628.2; DB 14; Length 1200;  
Best Local Similarity 80.3%; Pred. No. 1e-159;  
Matches 804; Conservative 0; Mismatches 178; Indels 19; Gaps 5;  
QY 1090 AGTTTCAGATTTTGAAGAAAGAAACAGTAATCTGTTCTGAGATTGAACCCAGAGAGGG 1149  
D 186 AATTTTCAGATTTTGAAGAAAGAAAGCAATGCGCATTTCTTACTGAGAGAGAGAGTGG 245  
QY 1150 GAGCAGAGAGAGAGAGAAATGATGAAGAGAAAGGCCCGAGACTGTTGGAAGCGAAGTGA 1209  
D 246 GAGAGCAGACAGAGAGA---AGGAGGACAAAGGCCAAGAGAGTGTTCGAAGCGAAGTGA 302  
QY 1210 AGCACTGAACCTCAAGTGCATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAAAC 1269  
D 303 AACACTGAGCATTTCAAGTGACCTCTCTGTTTAAAGAGCTTCAAGAGGACACACAAAAC 362  
QY 1270 CAGCGAGCTGAGCTTAATGAAGAGAGAGACTTCAAGAAAGTGTTCAGGCCCTTGAAGAG 1329  
D 363 CAGTGAGGCTGAGCTGATGAAGAGAGAGACTTCAAGAAAGTGTTCAGGCTCTGGAGAG 422  
QY 1330 AAATTTCTGCAATTTCCATCAGAGTTGAATGAAAGCAAGAGAGCTGTTTATATACAAAA 1389  
D 423 GAATCTGCAACACCATCAGAGCTGAATGAAAGCAGAGAGCTGTTTACAGTAAACAGAA 482  
QY 1390 GTTAGAGCTACAAAGTGGAAAGCATGCTATCAGAAATCAAAATGAAACAGAGCTTAAAC 1449  
D 483 GTTAGAGCTGAGTGGAGAGCATGCGCTCCGAAATCAAGATGGAGCAGGCCAAGACAGA 542  
QY 1450 GGATGAAAGTCCAAATTAATCTGTGTACAGATGACACACAAAGCTTCTTCAAGAAC 1509  
D 543 GGAGGAGAAAGTCCAGGTTAGCCACTCTGCGAGGCAACTCACAACAAGCTCTTCAAAA 602  
QY 1510 TAATAATGCATTGAAAGCAATTTGAGGAATCAACAAGAAAGAGTTCAGAAAA---GTGACA 1568  
D 603 TAATAAGGCCTGAAAGCAATTTGAGGAATCAACAAGCAAGAGCAAGAAAGAGTGGACA 662  
QY 1569 GGGCAGTGTCTGAAGGAACTGAGTGAAGAACTGGCAAGTGGCAGAGAGAGGCTCTGGCTTCCA 1628  
D 663 AATGTTGCTTGGCGAGCTCAGCGAAAGCTGGAGCTGGCAAGAGAGGCTCTGGCATCCA 722  
QY 1629 AACAGCTGCAATGGATGAAATGAAGCAACCAATTCGCAAGCAGAGAGAGAGAGCTGGAAA 1688  
D 723 AACAGCTCCAGATGGATGAGATGAAGCAGACGCTCGCTAAGCAGAGAGAGAGAGAGAG 782  
QY 1689 CCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAGAG 1748  
D 783 CCATGCGCGCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAGAG 842  
QY 1749 CAGCGAGAGAGAGAAATTCATGAGAAAGAGAGCAACTGGCATTTGCGAGCTGGCAGTTCTGC 1808  
D 843 CAGCAGAGAGAGAGATTCATGAGAAAGAGAGAGAGAGAGAGCTGGCTTGCAGCTCGCATTTGC 902  
QY 1809 TGAAGAGAGATGATGTTTTCGAAGACGGAGGC---AGGCAGTCTCTTATGAGAGAGAGAG 1865  
D 903 TGAAGAGAGAAATGACATTTGAAGAGGAGGAGGAGTAGACAGTCCCTGATGGAATGCA 962  
QY 1866 GTTCGTATGGGCGAGAAACAAAGTACTCTGACAGAGAGGCTTACCTTGTTCAGAGAGAG 1925  
D 963 GCGACACGCGGCAAGAACCAAGTACTCTGACAGAGAGAGTCTTACCTGTTTTCAGAGAG 1022  
QY 1926 CTGAGAGACAG-----GGACTGCGGCAACAGCGGAATATTCGAGTTCATTCCTGCC 1976



Db 1023 CCGAGGACAGGAGCTGGCAGCAGCGGGCAGCAGCCTCGCAGTATTCGGATTCACCTCTCGCC 1082

Qy 1977 CCAAGTGTGGAGAGGTTCTGCTCTGACATAGACACGCTTACAGATTTCACGCTGATGGATTGCA 2036

Db 1083 CCAAGTGTGGAGAGGTTCTGCTCTGCGGACATCGACAGCTTCAGATCCATGTGATGGACTGCA 1142

Qy 2037 TCATTTAAGTGTGATGATATCACCTCCCAAACTGTTGGT 2077

Db 1143 TCATTTAGTGT---TCTCTCAGTCCCCAAAGCTCTTGGT 1180

RESULT 33

ID ADL24739

AC ADL24739 standard; DNA; 815 BP.

XX ADL24739;

XX 20-MAY-2004 (first entry)

DE Intestinal epithelium/peyer's patch M cell-associated DNA sequence #75.

DE Intestinal epithelium cell development; peyer's patch M cell development;

XX inflammatory bowel disease; glutenenteropathy; infectious disease;

XX autoimmune disease; haemolytic anaemia; rheumatoid arthritis; dermatitis;

KW Grave's disease; multiple sclerosis; allergy; asthma; diabetic mellitus;

KW immune system disorder; hypersensitivity; anaphylaxis;

XX blood group incompatibility; ds; mouse; murine.

XX Mus musculus.

XX WO200280852-A2.

XX 17-OCT-2002.

XX 04-APR-2002; 2002WO-US010873.

XX 04-APR-2001; 2001US-0281416P.

XX (DIGI-) DIGITAL GENE TECHNOLOGIES INC.

XX Brayden DJ, Byrne D, O'mahony DJ, Evans CF, Mah SP, Lo DD;

PI WPI; 2003-075470/07.

XX Novel isolated or purified polypeptide encoded by genes associated with

PT intestinal epithelium or M cell development, differentiation or function,

PT useful for treating autoimmune diseases and infectious diseases.

XX Claim 1; SEQ ID NO 249; 152pp; English.

PS The invention comprises DNA sequences which are associated with

XX intestinal epithelium and peyer's patch M cells. The DNA sequences of the

CC invention are useful for assessing, modifying, modulating or regulating

CC intestinal epithelium or M cell development. The DNA sequences of the

CC invention are also useful in the treatment of: inflammatory bowel

CC disease, glutenenteropathy, infectious diseases, autoimmune diseases

CC (e.g. haemolytic anaemia, rheumatoid arthritis, dermatitis, Grave's

CC disease, multiple sclerosis, allergy, asthma and diabetic mellitus),

CC diseases or disorders of the immune system, hypersensitivity,

CC anaphylaxis, and blood group incompatibility. The present nucleic acid

CC represents an intestinal epithelium/peyer's patch M cell-associated DNA

CC sequence of the invention. NOTE: The present sequence is not shown in the

CC specification, but has been retrieved from the WIPO website.

XX Sequence 815 BP; 259 A; 195 C; 238 G; 133 T; 0 U; 0 Other;

Qy Query Match 26.2%; Score 544; DB 10; Length 815;

Db Best Local Similarity 81.9%; Pred. No. 6.5e-137;

Matches 668; Conservative 0; Mismatches 135; Indels 13; Gaps 3;

Qy 1213 ACTGAACCTCCAGTGCATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAACTCAG 1272

Db 1 ACTGAGCATTCAGTGCATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAACTCAG 60

Qy 1273 CGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCCCTTTGAAAGGAAAAA 1332

Db 61 TGAGGCTGAGCTGATGAAGAAAGAGACTTCAAGAAAAGTGTGAGGCCCTTTGAGAGAGAAA 120

Qy 1333 TTCTGCAATTCATCAGAGTGAATGAAGAAAGCAAGAGCTGTTTATCTAAACAAAAGTT 1392

Db 121 CTCTGCAACCATCAGAGCTGAATGAAGAAAGCAAGAGCTGTTTACAGTAAACAGAGTT 180

Qy 1393 AGAGCTACAAGTGGAAAGCATCTATCAGAAATCAAAATGGAAACAGGCTTAAACAGAGGA 1452

Db 181 AGAGCTGAGGTGGAGAGCATGCGCTCCGAAATCAAGATGGAGCAGGCCCAAGCAGAGA 240

Qy 1453 TGAAAAATCCAAATTAATCTGTGCTACAGATGACACAAACAGAGCTTCTCAAGAACATAA 1512

Db 241 GGAGAAATCCAGGTTAGCCACTCTCGAGGCAACTCACAAACAGCTCTTCAAGAACATAA 300

Qy 1513 TAATGCATTGAAACCAATTTAGGAACTAACAGAAAAGAGTTCAGAAAAGTGGACAGGGC 1572

Db 301 TAAGGCACCTGAAAACAATTTGAAGAACTAACAGCAACAGGCAGAAAAGTGGACAGAT 360

Qy 1573 AGTGTCTGAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACA 1632

Db 361 GTTGTCTGAGGAGCTCAGCGAGAAGCTGGAGCTGGCAGAGCAGGCTCTGGCATCCAAACA 420

Qy 1633 GCTGCAATGAGTGAATGAAGCAAAACATTTCCAGAGCAGGAGGAGGACCTGGAACCAT 1692

Db 421 GCTCCAGATGGATGAGATGAAGCAGACGCTCGCTAAGCAGGAGGAGACCTGGAGACCAT 480

Qy 1693 GACCATCTCAGGCTCAGATGGAAGTTTACCTGTTCTGATTTTTCATGCTGAAAGAGCAGC 1752

Db 481 GCGCGTCTCAGGCTCAGATGGAAGTTTACCTGTTCTGATTTTTCATGCTGAAAGAGCAGC 540

Qy 1753 GAGAGAGAAAATTCATGAGAAAAGAGCAACTGGCAATTCAGCTGGCAGTCTGCTGAA 1812

Db 541 AAGAGAGAGATTCATGAG- AAGAGAGCAGCTGGCTTGCAGTCTGCGATTTGCTGAA 599

Qy 1813 AGAGATGATGCTTTTGAAGAGCGAGGC---AGGAGTCTTGTAGTGGAGATGAGAGTCG 1869

Db 600 AGAGAACATGACATTTGAAGAGGAGGAGCAGTACAGTCCCTGATGAAATTCAGTGGCCG 659

Qy 1870 TCATGGGCGGAGAACAGTGACTCTGACCAGCAGGCTTACCTTGTTCAAAGAGGAGCTGA 1929

Db 660 ACACGGGGGCAAGAACAGTGACTCTGACCAGCAGACTTACCTGTTTCAAAGAGAGCCGA 719

Qy 1930 GGACAG-----GGACTGGCGGCAACAGCGGAATATTCGATTCATTCTCTGCCCCAA 1980

Db 720 GGACAGGAGCTGGCAGCACGGGAGCAGCCTCGAGTATTCGATTCACCTCTCTGCCCAA 779

Qy 1981 GTGTGAGAGGTTCTGCTGACATAGACACGTTACA 2016

Db 780 GTGCGGGAGGTTCTGCTGCGGACATCGACACGTTCA 815

RESULT 34

AAH57391/C

ID AAH57391 standard; cDNA; 3454 BP.

XX AAH57391;

XX 10-SEP-2001 (first entry)

DE Human skeletal muscle cell specific cDNA sequence SEQ ID NO:231.

XX Human; tissue specific; diagnosis; brain; heart; skeletal muscle; lung;

KW liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss;

KW metabolic disease; developmental disease; cytostatic; immunomodulatory;

XX neuroprotective; gene therapy; cancer; immunopathology; neuropathology.

XX Homo sapiens.

XX WO200132927-A2.

PN

XX

PD 10-MAY-2001.  
XX 02-NOV-2000; 2000WO-US030396.  
XX 04-NOV-1999; 99US-0163508P.  
XX (INCY-) INCYTE GENOMICS INC.  
XX Sornase T, Seilhamer JJ, Watson GA;  
XX WPI; 2001-291057/30.  
XX New cell and tissue specific polynucleotides useful for diagnosis,  
XX prognosis or monitoring of treatments for disorders where the gene is  
XX associated with a cancer, immunopathology or neuropathology.  
XX Claim 1; Page 159-160; 327pp; English.  
XX  
XX AAH57161 to AAH57576 represent cell and tissue specific polynucleotide  
XX sequences (I). (I) can have cytostatic, immunomodulatory and  
XX neuroprotective activities, and can be used in gene therapy. (I) and  
XX proteins (II) encoded by then are used in high throughput screening  
XX assays to select DNA molecules, RNA molecules, peptide nucleic acids,  
XX mimetics, peptides, proteins, agonists, antagonists, antibodies or their  
XX fragments, immunoglobulins, inhibitors, drug compounds and pharmaceutical  
XX agents. Expression of (I) in a sample indicates the differentiation of  
XX embryonic stem cells into a tissue selected from brain, heart, kidney,  
XX liver, lung, skeletal muscle or pancreatic tissues. (I) and (II) are used  
XX to produce an expression profile that defines a metabolic or  
XX developmental process, treatment, condition, disease or disorder. The  
XX gene profile can be used for diagnosis, prognosis or monitoring of  
XX treatments and for investigating a predisposition to a disorder where the  
XX gene is associated with a cancer, immunopathology or neuropathology  
XX  
XX Sequence 3454 BP; 1094 A; 725 C; 794 G; 841 T; 0 U; 0 Other;  
XX  
XX Query Match 25.4%; Score 526.6; DB 4; Length 3454;  
XX Best Local Similarity 99.1%; Pred. No. 7.5e-132;  
XX Matches 540; Conservative 0; Mismatches 4; Indels 1; Gaps 1;  
XX  
XX 1307 AAGTGTGAGGCTTGAAGGAAATTCGCAATCCATGAGTGAATGAAGCA 1366  
XX 2549 AGTGTGAGGCTTGAAGGAAATTCGCAATCCATGAGTGAATGAAGCA 2490  
XX 1367 GAGCTTGTATTAACAACAAAGTTAGAGCTACAAGTGAAGCAATGCTATCAGAAATC 1426  
XX 2489 GAGCTTGTATTAACAACAAAGTTAGAGCTACAAGTGAAGCAATGCTATCAGAAATC 2431  
XX 1427 AAAATGGAACAGGCTAAACACAGAGGATGAAAGTCCAAATTAATGTGTACAGATGACA 1486  
XX 2430 AAAATGGAACAGGCTAAACACAGAGGATGAAAGTCCAAATTAATGTGTACAGATGACA 2371  
XX 1487 CACAAAGCTTCTTCAAGACATATAATGCAATGAAACCAATGAGGAACCTAACAGA 1546  
XX 2370 CACAAAGCTTCTTCAAGACATATAATGCAATGAAACCAATGAGGAACCTAACAGA 2311  
XX 1547 AAAGAGTTCAGAAAAGTGGACAGGCGAGTGTGTAAGGAATGAGTGAAGTGAAGTGAAGT 1606  
XX 2310 AAAGAGTTCAGAAAAGTGGACAGGCGAGTGTGTAAGGAATGAGTGAAGTGAAGTGAAGT 2251  
XX 1607 GCAGAGAGGCTCTGGCTTCCAAACAGCTGCAATGCAATGCAATGCAATGCAATGCAATG 1666  
XX 2250 GCAGAGAGGCTCTGGCTTCCAAACAGCTGCAATGCAATGCAATGCAATGCAATGCAATG 2191  
XX 1667 AACGAGAGGAGGCTGGAACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1726  
XX 2190 AAGCAGAGAGGAGGCTGGAACCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 2131  
XX 1727 TCTGATTTTTCATGCTGAAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGGAGCAACTG 1786  
XX 2130 TCTGATTTTTCATGCTGAAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGGAGCAACTG 2071  
XX 1787 GCATTGAGCTGGCAGTCTGCTGAAAGAGAGATGATGCTTTTCGAAGACGAGGAGCGAGCAG 1846

Db 2070 GCATTGAGCTGGCAGTCTGCTGAAAGAGAGATGATGCTTTTCGAAGACGAGGAGCGAG 2011  
Qy 1847 TCCTT 1851  
Db 2010 AACCT 2006  
RESULT 35  
ACD92914  
ID ACD92914 standard; cDNA; 685 BP.  
XX ACD92914;  
AC ACD92914;  
XX 23-SEP-2003 (first entry)  
XX Human colon cancer cell expressed cDNA #1326.  
XX  
XX Open reading frame detection; genome sequencing; colon cancer;  
XX breast cancer; population genome analysis; genetic shift; cancer;  
XX antibiotic resistance; antibiotic non-tolerance; congenital disease;  
XX agriculture; food crop genome; resistance gene; retrovirus;  
XX influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;  
XX gene; ss.  
XX  
XX Homo sapiens.  
XX US2002155438-A1.  
XX 24-OCT-2002.  
XX 27-SEP-1999; 99US-00406117.  
XX 20-NOV-1998; 98US-00196716.  
XX (SIMP/) SIMPSON A J G.  
XX (NETO/) NETO E D.  
XX (BRENT/) BRENTANI R R.  
XX Simpson AJG, Neto ED, Brentani RR;  
XX WPI; 2003-182626/18.  
XX  
XX Determining open reading frames of genome of an organism e.g. a human  
XX suffering from cancer involves use of single oligonucleotide primer at  
XX low stringency for preparing single-stranded cDNA from mRNA of  
XX individual.  
XX  
XX Example 9; Page 205-206; 959pp; English.  
XX  
XX The invention describes a method of determining open reading frames in  
XX the genome of organism, comprising contacting mRNA from cell of organism  
XX with a single oligonucleotide primer (I) at low stringency, preparing  
XX single-stranded cDNA by reverse transcribing mRNA with (I), amplifying  
XX cDNA, sequencing the product, and repeating the contacting, preparing  
XX and amplifying steps with different primers and sequencing resulting  
XX nucleic acids. The method is useful for: determining that a known  
XX nucleotide sequence from a genome of an organism corresponds to a  
XX nucleotide sequence of an open reading frame; for preparing a contig,  
XX nucleic acid molecule from a genome of an organism; and for sequencing  
XX all or part of a genome of an organism. mRNA is obtained from mammalian  
XX or human cell which is associated with a pathological condition e.g. a  
XX colon cancer or breast cancer cell. The method is useful for analyses of  
XX populations of subjects and can be used to carry out genetic analyses of  
XX large or small populations. further, it can be used to study living  
XX systems to determine if, e.g. there have been genetic shifts which render  
XX an individual or population more or less likely to be afflicted with  
XX diseases such as cancer, to determine antibiotic resistance or non-  
XX tolerance, and so forth. The method can also be used in the study of  
XX congenital diseases, and the risk of affliction to a foetus, as well as  
XX the study of whether the conditions are likely to be passed on to offspring  
XX through ova or sperm. The analyses for pathological conditions can be  
XX carried out in all animals, plants, birds, fish, etc. Using this method,

CC in the area of agriculture, for example the genomes of food crops can be  
CC studied to determine if resistance genes are present, defects in plant  
CC genomes can also be studied in this way. Similarly, the method permits  
CC determination of the pathogens which integrate into the genome, such as  
CC retroviruses and other integrating viruses such as influenza virus, have  
CC undergone shifts or mutations, which may require different approaches to  
CC therapy. This method is also applied to eukaryotic pathogens, such as  
CC trypanosomes, different types of Plasmodium, etc. The method essentially  
CC eliminates sequencing of non-coding portions. This sequence represents a  
CC polynucleotide isolated from human colon cancer cell cDNA library  
XX  
SQ Sequence 685 BP; 259 A; 114 C; 172 G; 132 T; 0 U; 8 Other;

Query Match 24.7%; Score 513.4; DB 10; Length 685;  
Best Local Similarity 98.1%; Pred. No. 1.2e-128;  
Matches 561; Conservative 0; Mismatches 7; Indels 4; Gaps 4;  
QY 956 AGCAGATCTGCAGATGGGCGCCAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAG 1015  
Db |||||  
7 AGCGGATCTGCAGATGGGCGCCAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAG 66  
QY 1016 CTCCTGCTGCTTAAGGGAAGGGAATCAGAGGTGGAGACTTCAAGTTGCACCTCAAG 1075  
Db |||||  
67 CTCCTGCTGCTTAAGGGAAGGGAATCAGAGGTGGAGACTTCAAGTTGCACCTCAAG 126  
QY 1076 GAGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAACCAAGTAATCGTTCTGAGATTGAA 1135  
Db |||||  
127 GAGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAACCAAGTAATCGTTCTGAGATTGAA 186  
QY 1136 ACCCAGACAGAGGGGAGCAGAGAAAGAAATGATGAAGAAAGCCCGGAGACTGTT 1195  
Db |||||  
187 ACCCAGACAGAGGGGAGCAGAGAAAGAAATGATGAAGAAAGCCCGGAGACTGTT 246  
QY 1196 GGAAGCGAAGTGAAGCACTGAACTCCAGTCCAGTGCACATCTCTGTTTAAGGAGCTTCAAGAG 1255  
Db |||||  
247 GGAAGCGAAGTGAAGCACTGAACTCCAGTGCACATCTCTGTTTAAGGAGCTTCAAGAG 306  
QY 1256 GCTCATACAAAATCTCAGCGAAGCTGAGCTAATGAAGAAGAGACTTCAAGAAAAGTGTGAG 1315  
Db |||||  
307 GCTCATACAAAATCTCAGCGAAGCTGAGCTAATGAAGAAGAGACTTCAAGAAAAGTGTGAG 365  
QY 1316 GCCTTTGAAAGGAAAATTC-TGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGT 1374  
Db |||||  
366 GCCTTTGAAAGGAAAATTC-TGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGT 425  
QY 1375 TTATACTAACAAAAGTTAGAGCTACAAAGTGAAGCATCTATCAGAAATCAAAATGGA 1434  
Db |||||  
426 TTATACTAACAAAAGTTAGAGCTACAAAGTGAAGCATCTATCAGAAATCAAAATGGA 485  
QY 1435 ACAGGCTTAAACAGAGGATGAAAAGTCCAAATTAACCTGTCTACAGATGACACACAACAA 1494  
Db |||||  
486 ACA-GCTTAAACAGAGGATGAAAAGTCCAAATTAACCTG-NCTACAGATGACACACAACAA 543  
QY 1495 GCTTTCTCAAGAACATAAATGCAATTGAAAA 1526  
Db |||||  
544 GCTTTCTCAAGAACATAAATGCAATTGAAACA 575

RESULT 36  
ADF79591  
ID ADF79591 standard; DNA; 458 BP.  
XX  
AC ADF79591;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Leukaemia-related DNA sequence #147.  
XX  
KW Cytostatic; Gene therapy; leukaemia; ss.  
XX  
OS Unidentified.  
XX  
FN W02003039443-A2.

XX 15-MAY-2003.  
PD  
XX  
XX 04-NOV-2002; 2002WO-EP012303.  
PF  
XX  
XX 05-NOV-2001; 2001EP-00126244.  
PR  
XX  
XX 30-APR-2002; 2002EP-00009758.  
PR  
XX  
XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.  
PA (UYLU-) UNIV LUDWIG MAXIMILIANS.  
PA (HAFE/) HAFERLACH T.  
PA (SCHO/) SCHOCH C.  
PA (KERN/) KERN W.  
XX  
XX Haferlach T, Schoch C, Kern W, Kohlmann A, Schnittger S, Dugas M;  
PI Bils R, Brors B, Mergenthaler S;  
PI  
XX WPI; 2003-505037/47.  
DR  
XX  
XX Determining the subtype of leukemia cells and whether a patient sample  
PT contains leukemia cells or other cells, useful for treating leukemia,  
PT comprises determining the expression profile of a group of markers in a  
PT patient sample.  
XX  
XX Disclosure; SEQ ID NO 147; 2938pp; English.  
PS  
XX  
XX The present invention relates to a method (M1) for determining the  
CC subtype of leukaemia cells and whether a patient sample contains  
CC leukaemia cells. The method comprises determining the expression profile  
CC of a group of markers in a patient sample. The method is useful for  
CC determining the presence of leukaemia cells, its types or subtypes, and  
CC for the preparation of a medicament for treating leukaemia.  
XX  
SQ Sequence 458 BP; 135 A; 95 C; 130 G; 98 T; 0 U; 0 Other;  
Query Match 22.1%; Score 458; DB 10; Length 458;  
Best Local Similarity 100.0%; Pred. No. 1.2e-113;  
Matches 458; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1609 AGAGAAGGCTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATGCCAA 1668  
Db |||||  
1 AGAGAAGGCTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATGCCAA 60  
QY 1669 GCAGGAAGAGGACCTGGAAACCATGACCATCTCTCAGGCTCAGATGGAAGTTTACTGTTTC 1728  
Db |||||  
61 GCAGGAAGAGGACCTGGAAACCATGACCATCTCTCAGGCTCAGATGGAAGTTTACTGTTTC 120  
QY 1729 TGATTTTTCATGCTGAAAGAGCGAGAGAGAGAAATTCATGAGGAAAGAGCAACTGGC 1788  
Db |||||  
121 TGATTTTTCATGCTGAAAGAGCGAGAGAGAGAAATTCATGAGGAAAGAGCAACTGGC 180  
QY 1789 ATTGCAGCTGGCAGTTCTCTGCTGAAAGAGAAATGATGCTTTCGAGACGGAGGAGGAGTC 1848  
Db |||||  
181 ATTGCAGCTGGCAGTTCTCTGCTGAAAGAGAAATGATGCTTTCGAGACGGAGGAGGAGTC 240  
QY 1849 CTTGATGAGAGATCGAGAGTCGTCATGCGGCGAGAAACAAGTACTCTGACAGAGGCTTGA 1908  
Db |||||  
241 CTTGATGAGAGATCGAGAGTCGTCATGCGGCGAGAAACAAGTACTCTGACAGAGGCTTGA 300  
QY 1909 CCTTGTTCAAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCA 1968  
Db |||||  
301 CCTTGTTCAAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCA 360  
QY 1969 TTCCTGCCCCAAGTGTGGAGAGGTTCTGCTGACATAGACACGCTTACAGATTCACGTTGAT 2028  
Db |||||  
361 TTCCTGCCCCAAGTGTGGAGAGGTTCTGCTGACATAGACACGCTTACAGATTCACGTTGAT 420  
QY 2029 GGATTGCATCAATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2066  
Db |||||  
421 GGATTGCATCAATTAAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 458  
RESULT 37





QY 956 AGCAGATCTGAGATGGGGCCAGAAATTACTTGAACATGAGGAGTTAACTGTGAGCCAG 1015  
DB 1 AGCAAAATCTGCAGAGGTACCAGGAATTATGTGGAGTTTGAGGAATTAATCTGTGAGCCAG 60  
QY 1016 CTCTGCTGTGCTTAAGGGAAGGAATCAGAAAGTGGAGACTTGAAGTTGCACTCAAG 1075  
DB 61 CTCTGCTGATTTCTTAAGGGAAGGAATCAGAAAGTGGAGACTTGAAGTTGCTCCCTCAAG 120  
QY 1076 GAGGCCAAAGAAAGAGTTTTCAGATTTTGAAGAAAGAAACAAAGTAATCTGTTGAGATTGAA 1135  
DB 121 GAAGCCAAAGAAAGAAATTTCTGATTTTGAAGAAAGAAAGCAAGGATCAATCTGAGACTGAG 180  
QY 1136 ACCCAGACAGAGGGGACACAGAGAAAGAAATGATGAAGAGAAAGCCCGGAGACTGTT 1195  
DB 181 ACCCAGACAGAGGGGACACAGAGAAAGAAAGCAAGAGGAGAGAAAGACACCAAACTATT 240  
QY 1196 GGAAGCCAAAGTGAAGCACTGACCTCCAGGTGACATCTGTTTAAAGGACTTCAAGAG 1255  
DB 241 GGAAGTGAAGTGAAGCACTGACCTCCAGGTGACATCTGTTTAAAGGACTTCAAGAG 300  
QY 1256 GCTCATACAAAACCTCAGCAAGCTGAGCTAATGAAGAAAGACTTCAAGAAAGTGTGAC 1315  
DB 301 GCTCAGACGAACTCAGTGAAGCTGAGCTAATGAAGAAAGACTTCAAGAAAGTGTGAC 360  
QY 1316 GCCCTTGAAGGAAAGAAATTCGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGT 1375  
DB 361 GCCCTTGAAGGAAAGAAATTCGCAAGCCCATCAGAACTGAATGAAAGCAAGAGCTGTT 420  
QY 1376 TATACCTAACAAAAG 1390  
DB 421 TATAAAACAAAAG 435

RESULT 40  
ABX49269  
ID ABX49269 standard; cdNA; 416 BP.  
XX  
AC ABX49269;  
XX  
DT 21-FEB-2003 (first entry)  
XX  
DE Bovine EST associated with lactation/muscle/fat deposition #14434.  
XX  
KW Bovine; ss; EST; expressed sequence tag; lactation; LMFD;  
KW muscle deposition; fat deposition; genome mapping; gene identification;  
KW gene analysis; cattle breeding.  
XX  
OS Bos Taurus.  
XX  
PN US2002137139-A1.  
XX  
PD 26-SEP-2002.  
XX  
PF 24-SEP-2001; 2001US-00960352.  
XX  
PR 12-JAN-1999; 99US-0115707P.  
PR 11-JAN-2000; 2000US-00480902.  
XX  
PA (BYAT/) BYATT J C.  
PA (MATH/) MATHIALAGAN N.  
PA (TAON/) TAO N.  
PA (WARR/) WARREN W C.  
XX  
PI Byatt JC, Mathialagan N, Tao N, Warren WC;  
XX  
DR WPI; 2003-110599/10.  
XX  
PT New nucleic acid associated with lactation, and muscle and fat  
PT deposition, useful for genome mapping, gene identification and analysis,  
PT cattle breeding, or for genetically improving cattle.  
XX  
PS Claim 2; SEQ ID NO 14434; 245pp; English.

XX The invention relates to a purified nucleic acid molecule associated with  
CC lactation or muscle and fat deposition (designated LMFD), derived from  
CC cattle, and the LMFD nucleic acid can specifically hybridize to a second  
CC nucleic acid molecule comprising any of 1512 nucleotide sequences,  
CC appearing as ABX34836-ABX49947, or complements of them. Also included are  
CC ; (1) a transformed cell having a nucleic acid comprising an LMFD nucleic  
CC acid linked to a promoter and a 3' non-translated sequence that  
CC functions in the cell to cause termination of transcription and addition  
CC of polyadenylated ribonucleotides to a 3' end of the mRNA molecule; and  
CC (2) determining a level or pattern of a molecule in a bovine cell or  
CC tissue comprising: (a) incubating a marker nucleic acid (comprising any  
CC of the 1512 nucleic acid sequences or its complement or fragment) with a  
CC complementary nucleic acid molecule obtained from the bovine cell or  
CC tissue, where hybridization between the marker nucleic acid and the  
CC complementary nucleic acid permits the detection of the molecule; and (b)  
CC detecting the level or pattern of the complementary nucleic acid, where  
CC the detection of the complementary nucleic acid is predictive of the  
CC level or pattern of the molecule. The LMFD nucleic acid is used for  
CC determining a level or pattern of a molecule in a bovine cell or tissue.  
CC It is useful for genome mapping, gene identification and analysis, cattle  
CC breeding, preparation of constructs for use in cattle gene expression, or  
CC for genetically improving cattle. The present sequence is one of the  
CC 1512 bovine LMFD EST (expressed sequence tag) nucleic acids. Note: The  
CC present sequence was not shown in the specification but was obtained in  
CC electronic format from the USPTO web site:  
CC seqdata.uspto.gov/sequence.html?DocID=20020137139  
XX  
SQ Sequence 416 BP; 167 A; 75 C; 102 G; 72 T; 0 U; 0 Other;

Query Match 16.1%; Score 333.4; DB 8; Length 416;  
Best Local Similarity 87.7%; Pred. No. 8.1e-80;  
Matches 364; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 1001 TTAACCTGTGAGCAGCTCTCTGCTGCTTAAGGAAGGGAATCAGAGGTGGAGAGACTT 1060  
DB 2 TTAACCTGTGAGCAGCTCTCTGCTGCTTAAGGAAGGGAATCAGAGGTGGAGAGACTT 61  
QY 1061 GAAGTTTGCACTCAAGGAGGCCAAAGAAAGAGTTTTCAGATTTTCAAAGAAAGAAACAAGTAAT 1120  
DB 62 GAAGTTTGCCCTCAAGGAAGCCAAAGAAAGAAATTTCTGATTTTGAAGAAAGCAAGGAT 121  
QY 1121 CGTTCTTGAGATTGAAACCCAGACAGAGGGGAGCACAGAGAAAGAAATGATGAAGAGAAA 1180  
DB 122 CATCTGTGAGACTGAGACCCAGACAGAGAGGACACACAGAACAGAGAAAGAGAGAGAAA 181  
QY 1181 GGGCCGGAGACTGTTGGAAAGCGAAGTGGAGCACTGAACTCCAGGTGACATCTCTGTTT 1240  
DB 182 GACACCAAAACTATTGGAAAGTGAAGTGGAAACACTGAACTTCAGGTGACAAACCTGTTT 241  
QY 1241 AAGGAGCTTCAAGAGGCTCATACAAACTCAGCGAAGCTGAGCTAATGAGAGAGACTT 1300  
DB 242 AAGGAGCTTCAAGAGGCTCACAGAAACTCAGTGAAGCTGAGCTAATGAGAGAGACTT 301  
QY 1301 CAAGAAAAGTGTGAGGCCCTTGAAGGAAAAAATTTCTGCAATTCATCAGAGTTGAATGAA 1360  
DB 302 CAAGAAAAGTGTGAGGCCCTTGAAGGAAAAAATTTCTGCAAGCCCATCAGAACTGAATGAA 361  
QY 1361 AAGCAAGAGCTGTTTATTAATACTAACAAAAAGTTAGAGCTACAAGTGAAGAGCATGC 1415  
DB 362 AAACAGAGAGCTGTTTATTAATACTAACAAAAAGTTAGAGCTACAAGTGAAGAGCATGC 416

RESULT 41  
AED67129  
ID AED67129 standard; DNA; 364 BP.  
XX  
AC AED67129;  
XX  
DT 12-JAN-2006 (first entry)  
XX  
DE Human marker DNA sequence SEQ ID NO:55.  
XX

KW ds; selectable marker; biosensor; gynecological disorder; gynecological;  
KW genitourinary disease; gynecology and obstetrics; immunoassay;  
KW endometriosis; ovary tumor; cytostatic; endocrine disease; neoplasm;  
KW breast tumor; uterine cervix tumor; cancer.  
XX Homo sapiens.  
XX US2005239146-A1.  
XX 27-OCT-2005.  
XX 17-FEB-2005; 2005US-00060867.  
XX 04-DEC-2001; 2001US-00004587.  
XX (TAIN/) TAINSKY M.  
XX (DRAG/) DRAGHICI S.  
XX (CHAT/) CHATTERJEE M.  
XX Tainsky M, Draghici S, Chatterjee M;  
XX WPI; 2005-757147/77.  
XX P-PSDB; AED67130.  
XX New biosensor comprises detection means for detecting a presence of at  
PT least one marker indicative of a specific disease, useful for detecting  
PT the presence of diseases or diagnosing diseases, e.g. gynecological  
PT disease.  
XX Disclosure; SEQ ID NO 55; 119pp; English.  
XX The invention relates to a novel biosensor for use in detecting the  
CC presence of diseases, comprising a detector for detecting a presence of  
CC at least one marker indicative of a specific disease. The disease  
CC detected by the biosensor is a gynecological illness. The detection means  
CC is selected from an assay, a microarray, a macroarray, a slide, or a  
CC filter containing specific biomarkers of disease. Preferably, the  
CC detection means is an immunoassay. Preferably, the disease is a  
CC gynecological disease selected from endometriosis, ovarian cancer, breast  
CC cancer, cervical cancer, or primary peritoneal carcinoma. The targets are  
CC personalized to the individual receiving treatment. The biosensor is  
CC useful as for detecting the efficacy of a pharmaceutical. It is also  
CC useful as staging means for detecting the disease stage. The biosensor is  
CC useful for detecting the presence of diseases including gynecological  
CC diseases, e.g. endometriosis, ovarian cancer, breast cancer, cervical  
CC cancer, or primary peritoneal carcinoma. It can also be used for  
CC diagnosing cancer. The present sequence represents a marker DNA sequence  
CC that may be used in a biosensor of the invention.  
XX SQ Sequence 364 BP; 131 A; 52 C; 89 G; 67 T; 0 U; 25 Other;  
Query Match 15.9%; Score 330; DB 14; Length 364;  
Best Local Similarity 93.0%; Pred. No. 6.4e-79;  
Matches 330; Conservative 0; Mismatches 25; Indels 0; Gaps 0;  
QY 979 GAATTACTTCGAACATGAGGAGTTAACTGTGACCCAGCTCTCTCTGTGCTTAAGGAAGG 1038  
DB 10 GAATTACTTCGAACATGAGGAGTTAACTGTGACCCAGCTCTCTCTGTGCTTAAGGAAGG 69  
QY 1039 GAATCAGAGCTGGAGAGCTTGAAGTTGCATCAGGAGGCCAAGAAAGAGTTTCAGA 1098  
DB 70 GAATCAGAGCTGGAGAGCTTGAAGTTGCATCAGGAGGCCAAGAAAGAGTTTCAGA 129  
QY 1099 TTTTGAAGAAACCAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGACACAGA 1158  
DB 130 TTTTGAAGAAACCAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGACACAGA 189  
QY 1159 GAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTTGAAGCGAAGTGAAGCACTGAA 1218  
DB 190 GAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTTGAAGCGAAGTGAAGCACTGAA 249  
QY 1219 CCTCCAGGTGACATCTCTGTTTAAGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC 1278

Db 250 CCTNCAGGTGACATNTNTGTTTAAAGGCTTNAANAGGCTTNAACAAAACCTNANCAANC 309  
QY 1279 TGAGCTAATGAAGAAGACAGCTTCAAGAAAAGTGTCAGGCCCTTGAAGGAAAAAT 1333  
DB 310 TGANCTAATGAANAANANACTTNAANAANAANTGTNANGCCNTTGAANGNNAAT 364  
RESULT 42  
ADU14099  
ID ADU14099 standard; DNA; 493 BP.  
XX AC ADU14099;  
XX 27-JAN-2005 (first entry)  
XX Solid tumour prognosis gene seqid 4538.  
DE cytostatic; gene therapy; expression profile; solid tumour;  
KW peripheral blood mononuclear cell; PBMC; prognosis; ds.  
XX Unidentified.  
XX WO2004097052-A2.  
XX 11-NOV-2004.  
XX 29-APR-2004; 2004WO-US013587.  
XX 29-APR-2003; 2003US-0466067P.  
XX 23-JAN-2004; 2004US-0538246P.  
XX (AMHP ) WYETH.  
XX (STRA/) STRAHS A.  
XX Strahs A, Trepicchio WL, Burczynski ME, Twine NC, Slonim DK;  
XX Immerman F, Dörner AJ;  
XX WPI; 2004-804779/79.  
XX A method, useful for prognosing and treating solid tumor, comprises  
PT comparing an expression profile of a gene expressed in peripheral blood  
PT mononuclear cells to a reference expression profile of a gene.  
XX Disclosure; Page; 11pp; English.  
XX The invention describes a method comprising comparing an expression  
CC profile of at least one gene in a peripheral blood sample of a patient to  
CC at least one reference expression profile of the at least one gene, where  
CC the patient has a solid tumour, and each of the gene is differentially  
CC expressed in peripheral blood mononuclear cells (PBMCs) of a first class  
CC of patients as compared to PBMCs of a second class of patients, where  
CC both the first and second classes of patients have the solid tumour, and  
CC each of the first and second classes is a subcluster formed by an  
CC unsupervised clustering analysis of gene expression profiles in PBMCs of  
CC a population of patients who have the solid tumour, and where the  
CC majority of the first class of patients has a first clinical outcome, and  
CC the majority of the second class of patients has a second clinical  
CC outcome. Also described are: a system comprising (i) a memory or a  
CC storage medium including data that represent an expression profile of at  
CC least one gene in a peripheral blood sample of a patient who has a solid  
CC tumour, (ii) at least another storage medium including data that  
CC represent at least one reference expression profile of the gene, (iii) a  
CC program capable of comparing the expression profile to the reference  
CC expression profile, and (iv) a processor capable of executing the  
CC program, where expression levels of the gene in peripheral blood  
CC mononuclear cells of patients who have the solid tumour correlate with  
CC clinical outcomes of the patients; and a nucleic acid or protein array  
CC comprising concentrated probes for solid tumour prognosis genes, where  
CC each of the solid tumour prognosis genes is differentially expressed in  
CC PBMCs of a first class of patients as compared to PBMCs of a second class  
CC of patients, where both the first and second classes of patients have a  
CC solid tumour, and where the first class of patients has a first clinical  
CC outcome, and the second class of patients has a second clinical outcome.



CC The method, system, and array are useful for prognosing and treating  
CC solid tumours. This sequence represents a solid tumour prognosis gene of  
CC the invention. Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 493 BP; 101 A; 74 C; 97 G; 72 T; 0 U; 149 Other;

Query Match 15.0%; Score 312; DB 13; Length 493;  
Best Local Similarity 69.2%; Pred. No. 5.9e-74;  
Matches 334; Conservative 0; Mismatches 147; Indels 2; Gaps 2;

QY 1597 ACTGGAAGTGCAGAGAGGCTCTGGCTTCCAAACA-GCTCAATGGATGAATGAAGC 1655  
Db 1 ACTGGAAGTGCAGAGAGGCTCTGGCTTCCAAACANNNNNNNNNNNNNNNNNNN 60  
QY 1656 AAACCATTTGCCAGCAGAGAGGACCTGGAAACCATGACCAT-CCTCAGGGCTCAGATG 1714  
Db 61 NNNNNNNNNNCGAAGAGAGACCTGGAAACCATGACCATCNNNNNNNNNNNNNNN 120  
QY 1715 GAAGTTTACTGTCTGATTTTTCATGCTGAAAGAGCAGCAGAGAGAAATTCATGAGAA 1774  
Db 121 NNN 180  
QY 1775 AAGAGCAACTGGCATTCGACCTGGCAGTTCCTGCTGAAGAGATGATGCTTTCGAAGAC 1834  
Db 181 AAGAGCAACTGGCATTCGACCTGGCAGTTCCTGCTGAAGAGATGATGCTTTCGAAGAC 240  
QY 1835 GGAGCAGGAGCTCTTGATGGAGATGCAGAGTCTGATGGGCGGAGCAAGTGAATCT 1894  
Db 241 NNAGGCGAGAGTCTTGATGGAGATGCAGAGTCTGATGGGCGGAGCAAGTGAATCT 300  
QY 1895 GACCAGCAGGCTTACCTTGTTCAAAGAGAGAGCTGAGGACAGGAGTGGCGCAACAGCGG 1954  
Db 301 GACCAGCAGGCTTACCTTGTTCAAAGAGAGAGCTGAGGACAGGAGTGGCGCAACAGCGG 360  
QY 1955 AATATTCGATTCATTCCTGCCCCAAGTGGAGAGGTTTCCTGATGACATAGACACGTTA 2014  
Db 361 AATATTCGATTCATTCCTGCCCCAAGTGGAGAGGTTTCCTGATGACATAGACACGTTA 420  
QY 2015 CAGATTCAGTGGATTCATTCATTTAAGTGTGATGATATCACTCCCAAACTGTT 2074  
Db 421 CAGATTCAGTGGATTCATTCATTTAAGTGTGATGATATCACTCCCAAACTGTT 480  
QY 2075 GGT 2077  
Db 481 GGT 483

RESULT 43  
AEB53489  
ID AEB53489 standard; DNA; 493 BP.  
XX  
AC AEB53489;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE Human probe for epithelial cell DNA chip SEQ ID 448.  
XX

Probe; ss; endothelial cell; gene expression; DNA chip; Antiinflammatory;  
KW Vasotropic; Gastrointestinal-Gen.; Cytostatic; immunomodulator;  
KW Immunosuppressive; Antiarteriosclerotic; Neuroprotective; Nootropic;  
KW Ophthalmological; CNS-Gen; Gynecological; Hepatotropic; Antipsoriatic;  
KW Respiratory-Gen; Antiasthmatic; Antiallergic; Dermatological;  
KW Antibacterial; Respiratory-Gen.; Inflammation; atherosclerosis;  
KW transplant rejection; tumor; inflammatory bowel disease; psoriasis;  
KW reperfusion injury; respiratory distress syndrome; asthma;  
KW allergic rhinitis; dermatitis; bacterial meningitis; encephalitis;  
KW uveitis; leucocyte disorder; central nervous system disorders;  
KW Alzheimers disease; endometriosis; multiple sclerosis;  
KW alcoholic hepatitis; bacterial pneumonia; lung inflammation; pleurisy;  
KW chronic bronchitis; bronchiectasis; cystic fibrosis;  
KW chronic obstructive pulmonary disease; vasculitis; polyarteritis nodosa;

extracranial temporal arteritis; pre-eclampsia; autoimmune diseases.  
Homo sapiens.  
WO2005068655-A2.  
28-JUL-2005.  
14-JAN-2005; 2005WO-GB0000057.  
16-JAN-2004; 2004GB-00000976.  
(UYCA-) UNIV CAMBRIDGE TECH SERVICES LTD.  
Smith SK, Charnock-Jones DS, Print CG, Johnson NA;  
WPI; 2005-563988/57.  
Assessing tissue inflammatory response, by determining level of five transcripts e.g., glycerol kinase, interleukin-6 or proteins encoding transcripts in sample, and comparing abundance of transcripts/proteins with control sample.  
Claim 21; SEQ ID NO 448; 492pp; English.  
The invention relates to assessing (M1) a tissue inflammatory response, involving determining quantitatively the level of at least five transcripts of Table-1a e.g., glycerol kinase, Tumor necrosis factor (TNF)-inducible A20, insulin-like growth factor binding protein 6, interleukin (IL)-6 or proteins encoded by the transcripts, in a sample, and comparing the abundance of transcripts or proteins with a control sample. Also included are diagnosing (M2) a condition with a tissue inflammatory response (involving determining the abundance of endothelial cell-derived proteins encoded by at least five transcripts of Table-1a in a sample from a patient suspected of suffering from such a condition), a gene chip array (I) for carrying out (M1)/(M2) (comprising at least five nucleic acids suitable for detection of at least five transcripts of Table-1a, optionally a control specific for transcripts, and one or more controls for the gene chip), a gene chip array (II) for detection of at least five transcripts of Table-1a, a protein based assay (M3) suitable for carrying out (M1)/(M2) (for the assessment of at least five proteins encoded by transcripts of Table-1a, optionally a control specific for protein and/or optionally one or more control for the assay), an assay (M4) for determining a modulator of a tissue inflammatory response or their condition, use of a modulator (III) obtained by (M4) for the treatment of tissue inflammatory response or their conditions and a vector (IV) comprising a sequence encoding a transcript from of Table-1b provided in the specification. (M1) is useful for assessing a tissue inflammatory response. The sample comprises cells obtained from a site within a patient affected by a tissue inflammatory response. The cells are endothelial cell, or the sample is of patient blood, serum or urine, where the endothelial cells are human umbilical vein endothelial cells, human coronary artery endothelial cells, or human uterine microvascular endothelial cells. The control sample is obtained from endothelial cells from a tissue of patient, which is not affected by a tissue inflammatory response or obtained from a tissue demonstrating an inflammatory response in a patient at an earlier point in time. (M2) is useful for diagnosing a condition with tissue inflammatory response. The tissue inflammatory response is associated with an inflammatory disease, vasculitic syndrome, atherosclerosis or an associated disease, chronic transplant rejection, where the condition involves tumor growth. The inflammatory disease such as inflammatory bowel disorders, psoriasis, ischemic reperfusion, adult respiratory distress syndrome, asthma, allergic rhinitis, dermatitis, meningitis, encephalitis, uveitis, diseases involving leucocyte diapedesis, central nervous system inflammatory disorders, Alzheimer's, endometriosis, multiple sclerosis, multiple organ injury syndrome, alcoholic hepatitis, bacterial pneumonia, antigen-antibody complex mediated diseases, inflammation of the lung (including pleurisy, alveolitis, pneumonia, chronic bronchitis, bronchiectasis, cystic fibrosis and chronic obstructive pulmonary disease (COPD)), and vasculitis, polyarteritis nodosa, giant cell arteritis, microscopic polyarteritis, pre-eclampsia and autoimmune diseases. (III) is useful for the treatment of tissue inflammatory response or their condition as

CC above. The present sequence is a probe used in the gene chip of the  
CC invention to detect a human gene chosen from those appearing in table 1a  
CC (known genes).  
XX  
SQ Sequence 493 BP; 101 A; 74 C; 97 G; 72 T; 0 U; 149 Other;  
  
Query Match 15.0%; Score 312; DB 14; Length 493;  
Best Local Similarity 69.2%; Pred. No. 5.9e-74;  
Matches 334; Conservative 0; Mismatches 147; Indels 2; Gaps 2;  
  
QY 1597 ACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACA-GCTGCAAAATGGATGAATGAAGC 1655  
Db |||||||  
1 ACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACANNNNNNNNNNNNNNNNNNN 60  
  
QY 1656 AAACCATTCGCAAGAGAGGACCTGGAAACCATGACCAT-CCTCAGGGCTCAGATG 1714  
Db |||||||  
61 NNNNNNNNNNGCAGGAAGAGGACCTGGAAACCATGACCATCNNNNNNNNNNNNN 120  
  
QY 1715 GAAGTTTACTGTTCTGATTTTCATGCTGAAAGAGCAGCAGAGAGAAATTCATGAGAA 1774  
Db |||||||  
121 NNN 180  
  
QY 1775 AAGGAGCACTGCAATTCGAGCTGGCAGTTCTCTGCTGAAAGAGATGATGCTTTTCAAGAC 1834  
Db |||||||  
181 AAGGAGCACTGNNN 240  
  
QY 1835 GGAGCAGGAGCAGTCTTGTATGAGATGCAGAGTCGTATGGGGCGAGAACAACTGACTCT 1894  
Db |||||||  
241 NNAGGCAGGAGCAGTCTTGTATGAGATGCAGAGTCGTATGGGGCGAGAACAACTGACTCT 300  
  
QY 1895 GACAGCAGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGAGCTGGGGCAACAGCGG 1954  
Db |||||||  
301 GACAGCAGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGAGCTGGGGCAACAGCGG 360  
  
QY 1955 AATATTCGATTCATTCCTGCCCAAGTGCGAGAGGTTCTGCTGACATAGACAGTTA 2014  
Db |||||||  
361 AATATTCGATTCATTCCTGCCCAAGTGCGAGAGGTTCTGCTGACATAGACAGTTA 420  
  
QY 2015 CAGATTCACGTGATGATTCATCAATTAAGTGTGATGATATCACCTCCCAAACTGTT 2074  
Db |||||||  
421 CAGATTCACGTGATGATTCATCAATTAAGTGTGATGATATCACCTCCCAAACTGTT 480  
  
QY 2075 GGT 2077  
Db |||  
481 GGT 483  
  
RESULT 44  
ACH20402  
ID ACH20402 standard; cDNA; 432 BP.  
XX AC  
XX ACH20402;  
XX  
DT 13-OCT-2003 (first entry)  
XX  
DE Human adult liver cDNA #14.  
XX  
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;  
KW genome mapping; biodiversity; genetic disorder.  
XX  
OS Homo sapiens.  
XX  
PN US2003073623-A1.  
XX  
PD 17-APR-2003.  
XX  
PF 30-JUL-2001; 2001US-00918995.  
XX  
PR 30-JUL-2001; 2001US-00918995.  
XX  
PA (DRMA/) DRMANAC R T.  
PA (LABA/) LABAT I.  
PA (STAC/) STACHE-CRAIN B.

PA (DICK/) DICKSON M C.  
PA (JONE/) JONES L W.  
XX  
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX  
XX WPI; 2003-615964/58.  
XX  
XX New polynucleotide sequences obtained from various cDNA libraries, useful  
PT as hybridization probes, as oligomers for PCR, for chromosome and gene  
PT mapping, in the recombinant production of protein, or in generating  
PT antisense DNA or RNA.  
XX  
XX Claim 1; SEQ ID NO 7614; 44pp; English.  
XX  
CC The invention relates to an isolated polynucleotide comprising any one of  
CC 38043 cDNA sequences, appearing as ACH2789-ACH50831, whose sequence was  
CC determined by the technique of SBH (sequencing by hybridisation). Also  
CC included is a purified polypeptide comprising a sequence corresponding to  
CC a reading frame of the novel polynucleotide. The nucleic acid sequences  
CC are useful in diagnostics as expressed sequence tags (EST) for  
CC identifying expressed genes or for physical mapping of the human genome,  
CC in forensics, in assessing biodiversity, or in identifying mutations  
CC responsible for genetic disorders and other traits. The nucleotide  
CC sequences are also useful as hybridisation probes, as oligomers for PCR,  
CC for chromosome and gene mapping, in the recombinant production of  
CC protein, or in generating antisense DNA or RNA. The purified polypeptide  
CC is useful for generating antibodies specific for it. The present sequence  
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data  
CC for this patent did not form part of the printed specification, but was  
CC obtained in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20030073623  
XX  
SQ Sequence 432 BP; 120 A; 129 C; 121 G; 62 T; 0 U; 0 Other;  
  
Query Match 14.3%; Score 296.2; DB 9; Length 432;  
Best Local Similarity 99.0%; Pred. No. 1.1e-69;  
Matches 298; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 298 AGGAACCTTCGCAATGTCCTCATCAACCTCTCAGCTGCCTCACTGAAAAGAGGACAGCCC 357  
Db |||||||  
130 AGGAACCTTCGCAATGTCCTCATCAACCTCTCAGCTGCCTCACTGAAAAGAGGACAGCCC 189  
  
QY 358 CAGTGAAGACACAGGAATGGACCCCTCCCTGGCCCAACCTGACACGCTTTAC 417  
Db |||||||  
190 CAGTGAAGACACAGGAATGGACCCCTCCCTGGCCCAACCTGACACGCTTTAC 249  
  
QY 418 CCGGAGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCCAGCTGAAAGA 477  
Db |||||||  
250 CCGGAGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCCAGCTGAAAGA 309  
  
QY 478 AGCCATGAAGCTTAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCCTGGAC 537  
Db |||||||  
310 AGCCATGAAGCTTAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCCTGGAC 369  
  
QY 538 AGAAGAACAGAGGAAGAGCCAGTCTTTTGATATACAGAGCAAGAAAGAGAGCG 597  
Db |||||||  
370 AGAAGAACAGAGGAAGAGCCAGTCTTTTGATATACAGAGCATAGAGCAATAGAGCG 429  
  
QY 598 T 598  
Db 430 T 430  
  
RESULT 45  
AEE13195  
ID AEE13195 standard; DNA; 505 BP.  
XX  
XX AEE13195;  
AC  
DT 26-JAN-2006 (first entry)  
XX  
XX Hamster consensus sequence SEQ ID NO 2706.  
DE  
XX

KW	array; DNA sequencing; ds.
XX	Cricetulus griseus.
OS	WO2005111246-A1.
XX	24-NOV-2005.
PN	11-MAY-2005; 2005WO-US016880.
XX	11-MAY-2004; 2004US-0570425P.
PD	(AMHP ) WYETH.
PP	Melville MW, Charlebois TS, Mounts WM, Hann LE, Sinacore MS;
PR	Leonard MW, Brown EL, Miller CP, Lee GW;
PA	WPI; 2005-811678/82.
XX	
PT	Forming an oligonucleotide array directed toward an unsequenced organism
PT	comprises selecting oligonucleotide probes comprising a first set of
PT	oligonucleotide probes, each of which is specific for one of the template
XX	sequences.
PS	Claim 5; SEQ ID NO 2706; 68pp; English.
XX	
CC	The invention relates to a method of forming an oligonucleotide array
CC	directed toward an unsequenced organism comprises selecting
CC	oligonucleotide probes comprising a first set of oligonucleotide probes,
CC	each of which is specific for one of the template sequences. The method
CC	is useful for forming an oligonucleotide array directed toward an
CC	unsequenced organism. The array is useful for detecting the presence,
CC	absence, and/or quantity of expression levels of genes in a cell derived
CC	from an unsequenced organism. The present sequence represents a consensus
CC	sequence for undiscovered CHO cell genes.
XX	
SQ	Sequence 505 BP; 155 A; 122 C; 141 G; 87 T; 0 U; 0 Other;
Query Match	14.1%; Score 292.4; DB 14; Length 505;
Best Local Similarity	80.8%; Pred. No. 1.3e-68;
Matches 341;	Conservative 0; Mismatches 81; Indels 0; Gaps 0
Qy	289 CTTTTCACAGAACTTGCGAATGTGCCATCAACTCCTCAGCTGCTCATGAAGAAGGA 348 
Db	83 CTAAAGCGACGGACCCTGTTACCATGTGCCATCAACCTCCGAGCTGCCTGACTGAGAAGG 142
Qy	349 GGACAGCCCCAGTGAAGCACAGGNAATGGACCCCACCTGGCCACCCCAAACCTGGA 408 
Db	143 TGACAGGCTCTGTGAGACCCCGAGGAAATGAACCCCTTAATAAGGTTCACCCGAGCTGGA 202
Qy	409 CACGTTTTACCCGGAGAGCTGTGACGACATGAAGAGCTCTCTGACCAAGAACCCACA 468 
Db	203 CACATTCACTCTGAGNGATGCTGCAGCAATGAAGAACTCTCGTTGTGAACCACCA 262
Qy	469 GCTGAAGAAGCCATGAAGCTAAAATAATCAAGCCATGAAGGGAGATTGTAGGAGCTTTC 528 
Db	263 GCTGAAGAAGCCATGAAGCTAAACAATCAAGCCATGAAGGGAGATATGAGGAGCTTTC 322
Qy	529 GGCCTGCACAGAAAAA CHAAGGAGAAACGCCAGTTTTTTTGGATATACAGAGCAAGAAGC 588 
Db	323 AGCCTGGCGAGAGAAGCAGAAGGAAACGACAGTTGTTTGCACACAGAAACAAAGAAGC 382
Qy	589 AAAAGAGCGTCTAATGGCTTTGAGTCAAGAAATCAGAAATTTGAGGAAGAGCTTGGAAA 648 
Db	383 TAAGAAGCTCTGATGACCTTTGAGTTATGAATAATGAGAAACCTGAAGGTGGAGCTTGGAAA 442
Qy	649 ACTAAAAAGGGAAAATCAGAAAAGGTTCATCTGAGGAGCCCCACTGATGACTCCAGGCTTCCCAG 708 
Db	443 ACTAAGAGAGAGAGTCAGAAAAGCCATTTGAAGGCTCCATATGTGTGGCTCCAGGCTCCCAT 502
Qy	709 GG 710
Db	503 GG 504



```

PF 29-JUL-2003; 2003EP-00447201.
XX
XX 02-AUG-2002; 2002JP-00226612.
XX
XX (SYSM-) SYSMEX CORP.
XX
XX Kouchi Y, Masago A, Takahata T;
XX
XX WPI; 2004-146134/15.
XX
XX Gene assay for predicting future onset of glaucoma, particularly primary
XX open angle glaucoma or normal ocular tension glaucoma, comprises
XX detecting a mutation of at least one base of the optineurin gene.
XX
XX Example 1; SEQ ID NO 3; 31pp; English.
XX
XX The present sequence comprises exon 5 of the glaucoma-associated gene,
XX CC OPTN (optineurin) ADL14949. The invention relates to a gene assay method
XX for predicting future onset of primary open angle glaucoma and/or normal
XX ocular tension glaucoma. This involves detecting a mutation in the OPTN
XX gene coding sequence, specifically a substitution of G for A at position
XX 619 and/or a substitution of A for G at position 898 of the OPTN coding
XX sequence. The mutation(s) is detected using a nucleic acid amplification
XX method using primers specific for the different exons of the coding
XX sequence, including primers SF5 ADL14965 and SR5 ADL14966 for exon 5.
XX
XX SQ Sequence 1203 BP; 362 A; 207 C; 270 G; 364 T; 0 U; 0 Other;
XX
XX Query Match 9.9%; Score 206; DB 12; Length 1203;
XX Best Local Similarity 100.0%; Pred. No. 6.1e-45;
XX Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 475 AGAAGCCATGAAGCTAAATCAAGCCATGAAGGGAGATTTCGAGAGCTTTCGGGCTG 534
XX |
XX Db 499 AGAAGCCATGAAGCTAAATCAAGCCATGAAGGGAGATTTCGAGAGCTTTCGGGCTG 558
XX |
XX QY 535 GACAGAGAAACAGAGGAGAGAGCCAGTCTTTTGTAGATACAGAGCAAGCAAAAGA 594
XX |
XX Db 559 GACAGAGAAACAGAGGAGAGAGCCAGTCTTTTGTAGATACAGAGCAAGCAAAAGA 618
XX |
XX QY 595 GCCTCTAATGGCCTTGAGTCATGAGATGAGAAATTGAAGGAGAGCTTGGAAAACTAAA 654
XX |
XX Db 619 GCCTCTAATGGCCTTGAGTCATGAGATGAGAAATTGAAGGAGAGCTTGGAAAACTAAA 678
XX |
XX QY 655 AGGGAATCAGAAAGGTCATCTGAGG 680
XX |
XX Db 679 AGGGAATCAGAAAGGTCATCTGAGG 704
XX
XX RESULT 49
XX ID ADW86573
XX ADW86573 standard; DNA; 1203 BP.
XX
XX AC ADW86573;
XX
XX DT 21-APR-2005 (first entry)
XX
XX DE Human optineurin (OPTN) gene exon 5 Seq 3.
XX
XX KW glaucoma; optineurin; genetic marker.
XX
XX KW glaucoma; optineurin; ophthalmological; ds; ocular disease;
XX DNA amplification; genetic marker.
XX
XX OS Homo sapiens.
XX
XX PN JP2005034112-A.
XX
XX XX 10-FEB-2005.
XX
XX PF 29-JUL-2003; 2003JP-00281897.
XX
XX PR 02-AUG-2002; 2002JP-00226612.
XX
XX PR 30-JUN-2003; 2003JP-00188070.
XX
XX
XX (TOAI-) TOA IYO DENSHI KK.
XX
XX WPI; 2005-156038/17.
XX
XX Estimating risk of onset of glaucoma, involves analyzing mutation in any
XX one portion of Optic new phosphorous gene, and utilizing analyzed
XX mutation as index for estimating risk of onset of glaucoma.
XX
XX Example 1; SEQ ID NO 3; 13pp; Japanese.
XX
XX This invention relates to a novel method for estimating the risk of onset
XX of glaucoma. Specifically, it refers to a method that involves analyzing
XX a mutation in any one portion of an optineurin (OPTN) gene and utilizing
XX the analyzed mutation as an index for estimating the risk of onset of
XX glaucoma. The present invention describes oligonucleotides to detect
XX mutations that hybridize with one or more portions of the OPTN glaucoma
XX related gene. Accordingly, it provides oligos that detect AD19G and G898A
XX mutations in the human OPTN gene of patients at risk of developing
XX glaucoma, in particular primary open-angle glaucoma and/or normal tension
XX glaucoma. These mutations will not be present in a sample obtained from a
XX healthy person who is not at risk of onset of glaucoma. This
XX polynucleotide sequence is a human OPTN exon of the invention.
XX
XX SQ Sequence 1203 BP; 362 A; 207 C; 270 G; 364 T; 0 U; 0 Other;
XX
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XX Best Local Similarity 100.0%; Pred. No. 6.1e-45;
XX Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 475 AGAAGCCATGAAGCTAAATCAAGCCATGAAGGGAGATTTCGAGAGCTTTCGGGCTG 534
XX |
XX Db 499 AGAAGCCATGAAGCTAAATCAAGCCATGAAGGGAGATTTCGAGAGCTTTCGGGCTG 558
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XX QY 535 GACAGAGAAACAGAGGAGAGAGCCAGTCTTTTGTAGATACAGAGCAAGCAAAAGA 594
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XX |
XX Db 679 AGGGAATCAGAAAGGTCATCTGAGG 704
XX
XX RESULT 50
XX ID ADE13891
XX ADE13891 standard; DNA; 46951 BP.
XX
XX AC ADE13891;
XX
XX DT 29-JAN-2004 (first entry)
XX
XX DE Human optineurin gene.
XX
XX KW Human; optineurin; ds; gene; ophthalmological;
XX single nucleotide polymorphism; SNP; glaucoma;
XX progressive ocular hypertensive disorder; glaucoma related disorder.
XX
XX OS Homo sapiens.
XX
XX PH Key Location/Qualifiers
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XX FT variation replace(691,G)
XX FT /*tag= b
XX FT /*standard name= "Single nucleotide polymorphism"
XX FT variation replace(709,G)
XX FT /*tag= c
XX FT /*standard name= "Single nucleotide polymorphism"
XX FT variation replace(887,A)

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FT FT /\*tag= e  
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XX XX US2003190617-A1.  
XX XX  
XX XX 09-OCT-2003.  
XX XX  
XX XX 06-MAR-2002; 2002US-00091281.  
XX XX  
XX XX 06-MAR-2002; 2002US-00091281.  
XX XX (SIE/) SI E.  
XX XX (RAYM/) RAYMOND V.  
XX XX (MORI/) MORISSETTE J.  
XX XX  
XX XX Raymond V, Morissette J, Si E;  
XX XX WPI; 2003-864168/80.  
XX XX  
XX XX New nucleic acid sequences of the optineurin gene are useful to detect  
XX XX PT polymorphisms particularly single nucleotide polymorphisms in the  
XX XX PT optineurin promoter to diagnose, prognosis and treat glaucoma and related  
XX XX PT disorders.  
XX XX  
XX XX Disclosure; SEQ ID NO 2; 159pp; English.  
XX XX  
XX XX The invention relates to an isolated nucleic acid (N1) comprising at  
XX XX CC least 20 but not more than 1500 consecutive nucleotides of the optineurin  
XX XX CC promoter appearing as AD813890. Also included are the optineurin promoter  
XX XX CC operably linked to a heterologous nucleic acid, a nucleic acid capable of  
XX XX CC detecting a single nucleotide polymorphism (SNP) in the optineurin

CC promoter, a host cell comprising the promoter operably linked to a  
CC heterologous sequence, diagnosing or prognosing glaucoma in a sample  
CC obtained from a cell or bodily fluid (comprising detecting a polymorphism  
CC in a promoter region of the optineurin gene, associated with a glaucoma  
CC phenotype), detecting a SNP sequence variation in a sample containing  
CC DNA, detecting the presence of an optineurin promoter sequence variation  
CC in a sample containing DNA, determining the presence or increased  
CC susceptibility to glaucoma or to a progressive ocular hypertensive  
CC disorder resulting in loss of visual field in a patient (or the severity  
CC or progression of glaucoma in a patient, comprising providing  
CC amplification reaction primers that direct amplification of a selected  
CC nucleic acid region containing the variation within the optineurin  
CC promoter and amplifying the DNA) and detecting a polymorphism (comprising  
CC obtaining a sample containing human genomic DNA, providing a nucleic acid  
CC capable of detecting a SNP located within an optineurin promoter, and  
CC detecting the polymorphism). The invention is used to diagnose and  
CC prognose glaucoma and also to treat glaucoma related disorders. The  
CC present sequence is the optineurin gene.  
XX XX  
SQ Sequence 46951 BP; 12703 A; 10108 C; 10051 G; 14089 T; 0 U; 0 Other;  
Query Match 9.9%; Score 206; DB 10; Length 46951;  
Best Local Similarity 100.0%; Pred. No. 4.2e-44; Mismatches 0; Gaps 0;  
Matches 206; Conservative 0; Indels 0;  
QY 475 AGAAGCCATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTGGGCTG 534  
Db 15116 AGAAGCCATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTGGGCTG 15175  
QY 535 GACAGAGAAACAGAGAGGAAGAACGCCAGTTTTTTTGTAGATACAGAGCAAGAGCAAAAGA 594  
Db 15176 GACAGAGAAACAGAGAGGAAGAACGCCAGTTTTTTTGTAGATACAGAGCAAGAGCAAAAGA 15235  
QY 595 GCGTCTAATGGCTTTGAGTTCATGAGAAATGAGAAATTTGAAGGAGAGCTTTGGAATACTAAA 654  
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Db 15296 AGGGAATATCAGAAAGTTCATCTGAGG 15321

Search completed: May 30, 2006, 01:44:33  
Job time : 2353 secs

GenCore version 5.1.8  
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OM nucleic - nucleic search, using sw model

Run on: May 29, 2006, 23:56:43 ; Search time 8892 Seconds  
(without alignments)

13061.679 Million cell updates/sec

Title: SEQ1-458A

Perfect score: 2077

Sequence: 1 atccgggtcgggagttctct.....acctccccaaaactgattggt 2077

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 48236798 seqs, 27959665780 residues

Total number of hits satisfying chosen parameters: 96473596

Minimum DB seq length: 0

Maximum	DB seq	length:
Maximum	DB seq	length: 2000000000

Post-processing: Minimum March 03

**Post-processing: Minimum Match 0% Maximum Match 100%**

MAXIMUM MATCH 100%  
Listing first 150 summaries

Database :

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message ,
    est1:
    1: qb est1:*

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1: qb_est1: *
2: qb_est3: *
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3: gb\_est4: \*

4: gb\_est5: \*

5: gb\_est6: \*

6: gb\_htc:\*

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7: gb_est2:*
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12: gb\_gss2:\*

13: gb\_gss3: \*

14: gb\_gss4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	1770.8	85.3	1864	6	CR601600	full-leng
2	1738.8	82.7	1862	6	CR597026	full-leng
3	1710.8	82.4	1846	6	CR603260	full-leng
4	1426.2	68.7	3265	6	CR895973	Pongo pyg
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C 6	986.6	47.5	1089	4	BX384735	BX384735
C 7	982.6	47.3	1068	1	AL583163	AL583163
C 8	957.6	46.1	1032	1	AL570028	AL570028
C 9	937.2	45.1	1021	1	AL562864	AL562864
10	902.2	43.4	1004	1	AL553761	AL553761
C 11	882.4	42.5	1012	4	BX343673	BX343673
C 12	868.8	41.8	996	1	AL516921	AL516921
C 13	857.6	41.3	984	1	AL526184	AL526184
14	837.6	40.3	1001	1	AL583164	AL583164
15	824.4	39.7	1497	14	DQ036022	CR036022 Pan trogl
16	806.8	38.8	810	9	CX781622	HESCS_7_D
C 17	800	38.5	882	1	AL565248	AL565248
18	797	38.4	955	1	AL516922	AL516922
19	789.2	38.0	982	3	BU161830	AGENCOURT



93	557	26.8	569	9	DA973236	DA973236	DA973236
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95	553.4	26.6	700	2	BM083679	imagqc_2	
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c	98	542.8	592	4	CA445794	UI-H-ED0-	
	99	542.8	571	4	CB149479	K-EST0206	
	100	533.4	601	5	CD676203	fs3e02.y	
	101	533.2	687	4	CB984556	AGENCOURT	
	102	532.6	769	10	DV920362	LB02921.C	
	103	532.6	826	9	DN285973	1240031.M	
c	104	532.4	556	7	BF437125	7p63e08.x	
	105	532.2	583	3	BP358242	BP358242	
c	106	532.2	612	3	BM684554	UI-B-EJ0-	
	107	531	594	5	CD675512	fs24e01.y	
	108	531	805	4	BM984898	BW984898	
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	110	529	529	3	BM704972	UI-B-DW0-	
	111	528	528	9	DA312131	DA312131	
c	112	527.4	560	1	AI814613	wj75c08.x	
	113	526.8	762	8	CR856324	DKF2p469P	
	114	525	862	2	BI560200	60325334	
	115	524.4	1330	10	DV789814	Hw Liver	
	116	523.8	900	2	BI770911	603059723	
	117	523.6	765	5	CJ464429	CJ464429	
	118	522.2	826	2	BG427366	602494459	
	119	521.8	774	5	CJ483408	CJ483408	
	120	520.8	831	5	CJ474283	CJ474283	
c	121	520	555	9	DB341260	DB341260	
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	125	514.6	521	4	CB156457	K-EST0215	
	126	513.6	736	4	CB987407	AGENCOURT	
	127	513.4	685	1	AI907258	MR-BT137-	
c	128	513	548	1	AA808902	tw16c09.s	
	129	511	539	4	CB129346	K-EST0178	
	130	509.8	553	9	DA895737	DA895737	
c	131	508.8	580	7	AW167487	XG76f09.x	
	132	508	831	4	BM984065	BM984065	
	133	505.2	873	7	BF575959	602132935	
	134	504.6	722	3	BU928109	AGENCOURT	
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	146	495.8	582	3	BP236590	BP236590	
c	147	495.4	524	9	DB316715	DB316715	
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	149	494	609	1	AV647360	AV647360	
150	493	23.7	506	1	AA211559	zn55f09.r	

ALIGNMENTS

RESULT 1	CR601600	CR601600	1864 bp	mRNA	linear	HTC 21-JUL-2004
LOCUS	full-length cDNA clone CS0DC016YG04 of Neuroblastoma Cot	25-normalized of Homo sapiens (human).				
DEFINITION	CR601600	CR601600				
ACCESSION	CR601600.1	GI:50482407				
VERSION	HTC; CNSLT-CDNA.					
KEYWORDS	Homo sapiens (human)					
SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					

REFERENCE	1 (Bases 1 to 1864)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.
AUTHORS	Li.W.B., Gruber.C., Jessee.J. and Polayes.D.	
TITLE	Full-length cDNA libraries and normalization	
JOURNAL	Unpublished	
REMARK	Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue	
REFERENCE	2 (Bases 1 to 1864)	Genoscope.
AUTHORS	Direct Submission	
TITLE	Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :	
JOURNAL	BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr	
COMMENT	- Web : www.genoscope.cns.fr)	
	1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.	
FEATURES	Location/Qualifiers	
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QY	417 CCCCAGGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCCACAGCTGAAAG	476
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QY	657 GGAAATCAGAAAGGTCTATCTGAGGACCCCATGATGATCTCCAGGCTTCCAGGGCCGAAG	716
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QY	717 CGGAGCAGGAAGGACCCAGCTCAGAGCCCGAGTGTGAGGCTTACAGCAGAGAGGCGAG	776
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QY	777 ACCTGTTGGGCTTCGTGTGAACCTGCAGCTCAAGCTGAACCTCCAGCGCTCTCTCAGAAG	836
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Qy 1137 CCAGACAGAGGGGGGACACAGAGAGAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTG 1196
Db 931 CCAGACAGAGGGGGGACACAGAGAGAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTG 990
Qy 1197 GAAGCGAAGTGGAGACACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG 1256
Db 991 GAAGCGAAGTGGAGACACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG 1050
Qy 1257 CTCATACAAACTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGAGTGCAGG 1316
Db 1051 CTCATACAAACTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGAGTGCAGG 1110
Qy 1317 CCCTTGAAGGAAAAATCTGCATTTCCATCAGAGTTGAATGAAGAAAGAGAGCTGTTT 1376
Db 1111 CCCTTGAAGGAAAAATCTGCATTTCCATCAGAGTTGAATGAAGAAAGAGAGCTGTTT 1170
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Db 1231 AGGCTAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGC 1290
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Db 1471 AGGACCTGGAACCATGACCATCCTCAGGCTCAGATGGAAGTTACTGTTCTGATTTTC 1530
Qy 1737 ATGCTGAAGAGCAGCGAGAGAGAAAATTCATGAGAAAGAGGAACTGGCAATGAGC 1796
Db 1531 ATGCTGAAGAGCAGCGAGAGAGAAAATTCATGAGAAAGAGGAACTGGCAATGAGC 1590
Qy 1797 TGGCAGTTCTGTGAAAGAGAAATGATGCTTTCAAGACGGAGGAGCGAGTCTCTGATGG 1856
Db 1591 TGGCAGTTCTGTGAAAGAGAAATGATGCTTTCAAGACGGAGGAGCGAGTCTCTGATGG 1650
Qy 1857 AGATGAGAGTCTGATGGGGCGAGAACCAAGTGAATCTGACACGAGGCTTACTTGTTC 1916
Db 1651 AGATGAGAGTCTGATGGGGCGAGAACCAAGTGAATCTGACACGAGGCTTACTTGTTC 1710
Qy 1917 AAGAGGAGCTGAGGACAGGGAATGCGGGCAACAGCGGAATATTCGATTCATCTGCG 1976
Db 1711 AAGAGGAGCTGAGGACAGGGAATGCGGGCAACAGCGGAATATTCGATTCATCTGCG 1770
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Qy 1977 CCAAGTGTGAGAGGTTCTGCTGACATAGACAGTTTACAGATTCAAGTGTGATGATTGCA 2036
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Qy 2037 TCATTTAAGTGTGATGATATCACCTCCCAAAAC 2070
Db 1831 TCATTTAAGTGTGATGATATCACCTCCCAAAAC 1864

RESULT 2
CRS97026 1862 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CS0DL009Yf13 of B cells (Ramos cell line)
DEFINITION Cot 25-normalized of Homo sapiens (human).
ACCESSION CR597026
VERSION 1 GI:50477833
KEYWORDS HTC; CNSLT_cDNA..
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1862)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 1862)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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ORIGIN
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Best Local Similarity 99.9%; Pred. No. 0;
Matches 1740; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 297 CAGGAATCTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGAGACAGCC 356
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Qy 357 CCAGTGAAGACAGGAAATGGACCCCACTGGCCCAACCCCAACCTGGACACCGTTTA 416
Db 181 CCAGTGAAGACAGGAAATGGACCCCACTGGCCCAACCCCAACCTGGACACCGTTTA 240
Qy 417 CCCCGAGAGAGCTGCTGACGAGATGAAGAGCTCTGACCAAGAACCCACCTGAAAG 476
Db 241 CCCCGAGAGAGCTGCTGACGAGATGAAGAGCTCTGACCAAGAACCCACCTGAAAG 300
Qy 477 AAGCCATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCCTGGA 536
Db 301 AAGCCATGAAGCTAAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCCTGGA 360
Qy 537 CAGAGAAAACAGAGGAAGAACCGCAGTTTTCAGATACAGAGCAAGCAAGCAAGCAAGAGC 596
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Db	361	CAGAGAAACAGAGGAAGAACCCAGTTTCTTTTGTAGATACAGAGCAAAAGAACAAAGAGC	420
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Db	421	GTCTAATGCGCTTTGAGTCATGAGAAATGAGAAATGAGAAAGAGCTTTGAAAACCTAAAG	480
Qy	657	GGAAATCAGAAAGGTTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG	716
Db	481	GGAAATCAGAAAGGTTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG	540
Qy	717	CGAGCAGGAAAGGACCGAGCTCAGAACCCAGGTGTGAGGCTTCAAGCAGAGAGGCGAG	776
Db	541	CGAGCAGGAAAGGACCGAGCTCAGAACCCAGGTGTGAGGCTTCAAGCAGAGAGGCGAG	600
Qy	777	ACCTGTGGGCATCGTGTCTGAACTGCACTCAAGCTCAAGCTCAAGCTCCAGCGCTCCTCAGAG	836
Db	601	ACCTGTGGGCATCGTGTCTGAACTGCACTCAAGCTCAAGCTCCAGCGCTCCTCAGAG	660
Qy	837	ATTCTCTTTGTTGAAATTAGGATGGCTGAAAGGAGAACGAGAAAGGTTCAGTAAAGAAATCA	896
Db	661	ATTCTCTTTGTTGAAATTAGGATGGCTGAAAGGAGAACGAGAAAGGTTCAGTAAAGAAATCA	720
Qy	897	AGCATAGTCCTGGGCCACGAGAACAGTCTCACTGGCACCGCATTTGTTAAATATAGGA	956
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Qy	957	CGAGATCTCGAGATGGGGCCAGAAATTAATCTCGAACATGAGAGTTAACTGTGAGCCAGC	1016
Db	781	CGAGATCTCGAGATGGGGCCAGAAATTAATCTCGAACATGAGAGTTAACTGTGAGCCAGC	840
Qy	1017	TCTGTCTGTCCCTTAAGGGAAGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACCTCAAGG	1076
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Qy	1197	GAGCGAAGTGGAGCACTGAACTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGG	1256
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Qy	1317	CCCTTGAAGGAAAAATTCGCAATTCATCAGAGTTGAATGAAGAAAGAGCTTGTGTT	1376
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Qy	1377	ATACTAACAAAAAGTTAGAGCTACAAAGTGAAGCAATGCTATCAGAAAACTCAAAATGGAAC	1436
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Qy	1437	AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGC	1496
Db	1261	AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGC	1320
Qy	1497	TTCTTCAAGAACATATATGCAATGAAACANTTGAAGCACTTAAAGAAAGAGCTCAG	1556
Db	1321	TTCTTCAAGAACATATATGCAATGAAACANTTGAAGCACTTAAAGAAAGAGCTCAG	1380
Qy	1557	AAAAAGTGACAGGGCAGTGCTGAAAGAACTGAGTGAAGAACTGGAACTGGCAGAGG	1616
Db	1381	AAAAAGTGACAGGGCAGTGCTGAAAGAACTGAGTGAAGAACTGGAACTGGCAGAGG	1440
Qy	1617	CTCTGGCTTCCAAACAGCTGCAAAATGGATGAATGAAGCAAACTATGCGCAAGCAGGAG	1676
Db	1441	CTCTGGCTTCCAAACAGCTGCAAAATGGATGAATGAAGCAAACTATGCGCAAGCAGGAG	1500
Qy	1677	AGGACTGTGAACCACTGACCATCTCAGGGCTCAGATGGAAGCTTACTGTCTGATTTTC	1736
Db	1501	AGGACTGTGAACCACTGACCATCTCAGGGCTCAGATGGAAGCTTACTGTCTGATTTTC	1560
Qy	1737	ATGCTGAAGAGCAGCGAGAGAGAAAATTCATGAGAAAAGAGCAACTGGGATTGCAGC	1796
Db	1561	ATGCTGAAGAGCAGCGAGAGAGAAAATTCATGAGAAAAGAGCAACTGGGATTGCAGC	1620
Qy	1797	TGGCAGTTCTGCTGAAAGAGATGATGCTTTCGAAAGCGAGCGAGGAGCTCTTCATGG	1856
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Qy	1857	AGATCGAGAGTCGTCTCATGGGCGAGAAACAAGTGAATCTCACCAGCAGGCTTACCTTGTTC	1916
Db	1681	AGATCGAGAGTCGTCTCATGGGCGAGAAACAAGTGAATCTCACCAGCAGGCTTACCTTGTTC	1740
Qy	1917	AAAGAGGAGCTGAGACAGGGACTGGCGGCAACACGCGGAATATTCGATTTCATTCCTGCC	1976
Db	1741	AAAGAGGAGCTGAGACAGGGACTGGCGGCAACACGCGGAATATTCGATTTCATTCCTGCC	1800
Qy	1977	CCAAGTGTGGAGAGCTTCTGCTGACATAGACACGCTTACAGATTACCTGATGGATTGCA	2036
Db	1801	CCAAGTGTGGAGAGCTTCTGCTGACATAGACACGCTTACAGATTACCTGATGGATTGCA	1860
Qy	2037	TC 2038	
Db	1861	TC 1862	
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full-length cDNA clone CS0D1003YG24 of Placenta Cot 25-normalized			
of Homo sapiens (human).			
CR603260			
ACCESSION			
CR603260.1 GI:50484067			
VERSION			
HTC; CNSLT cdna.			
KEYWORDS			
Homo sapiens (human)			
SOURCE			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
REFERENCE			
1 (bases 1 to 1846)			
Li W.B., Gruber, C., Jessee, J. and Polayes, D.			
Full-length cDNA libraries and normalization			
AUTHORS			
Unpublished			
JOURNAL			
REMARK			
Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitrogen Corporation 1600 Faraday Avenue			
REFERENCE			
2 (bases 1 to 1846)			
Genoscope.			
Direct Submission			
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :			
Bp 191 91006 BVRV cedex - FRANCE (E-mail : seqref@genoscope.cns.fr			
- Web : www.genoscope.cns.fr)			
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime			
end enriched, double-strand cDNA was digested with Not I and cloned			
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library			
was normalized. Library was constructed by Life Technologies, a			
division of Invitrogen.			
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Best Local Similarity 98.9%; Pred. No. 0;			

Matches 1740; Conservative 0; Mismatches 2; Indels 18; Gaps 1;			
Qy	297	CAGGAACTTCTGCAATGCCCATCAACCTCTCAGCTGCTCAGTGAAGAGGAGGACGAC	356
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Qy	357	CCAGTGAAGCAGAGGAATGGACCCGCCACCTGGCCACCCCAAACTTGAGACAGTTTA	416
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Qy	417	CCCCGAGGAGCTCTCAGCAGATGAAGAGCTCTGACCAGCAAGAACCCAGCTGAAAG	476
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Qy	477	AAGCCATGAAGCTAAATTAATCAAGCCATGAAGAGGAGATTGAGGAGCTTTCCGCCCTGGA	536
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Qy	537	CAGAGAACAGAGGAAGAGCGCCAGTTTGTGATACAGAGCAAGAGCAAGAGAGC	596
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Qy	717	CGAGCAGGAAGAGGACAGCTCAGGACCCAGAGTGTGAGGCTTACAAGCAGAGAGCGAG	776
Db	525	CGAGCAGGAAGAGGACAGCTCAGGACCCAGAGTGTGAGGCTTACAAGCAGAGAGCGAG	584
Qy	777	ACCTGTTGGGCATCGTCTGAACTGAGCTCAAGCTGAATCCAGCGGCTCCTCAGAAG	836
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Qy	837	ATTCTTTGTTGAAATPAGGATGGCTGAAGGAGAGCAGAGGCTCAGTAAAGAAATCA	896
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Qy	897	AGCATAGTCTGGGCCACAGAGACAGTCTCCACTGGCAGCGCATGCTTAAATATAGGA	956
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Qy	957	GCAGATCTGCAGATGGGGCCAGAAATTAATCTGCAACATGAGGATTAATCTGTAGCCAGC	1016
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Db	987	GAAGCGAAGTGGAGACACTGAACTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGG	1046
Qy	1257	CTCATCAAAACTCAGCGAAAGCTAGCTAATGAAGAGAGACACTTCAAGAAAGTGTCAAG	1316
Db	1047	CTCATCAAAACTCAGCGAAAGCTAGCTAATGAAGAGAGACTTCAAGAAAGTGTCAAG	1106
Qy	1317	CCCTTGAAGGAAAAATCTGCAATTCATCAGAGTTGAATGAAGACAGAGCTTGT	1376
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Qy	1377	ATACTAACAAAAAGTTAGAGCTACAAGCTGGAAAGCATGCTATCAGAATCAAAATGGAC	1436
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Qy	1437	AGGCTAAAAACAGAGGATGAAAAGTCCAAAATTAACGTGTCTACAGATGACACACAAGC	1496
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Db	1347	AAAAAGTGGACAGCGCAGTGTCTGAAGGAACTGAGTGAAAAAATCTGGAACTGGCAGAGAAG	1406
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Qy	1677	AGGACCTGGAAACCATGACCATCTCAGGCTCAGATGGAAGTCTTACTGTCTGATTTTC	1736
Db	1467	AGGACCTGGAAACCATGACCATCTCAGGCTCAGATGGAAGTCTTACTGTCTGATTTTC	1526
Qy	1737	ATGCTGAAAGCAGCAGCGAGAGAGAAAAATTCATGAGGAAAAAGGAGCAACTGGCAATTGCAGC	1796
Db	1527	ATGCTGAAAGCAGCAGCGAGAGAGAAAAATTCATGAGGAAAAAGGAGCAACTGGCAATTGCAGC	1586
Qy	1797	TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGAGGAGGAGGAGTCTTGTATGG	1856
Db	1587	TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGAGGAGGAGGAGTCTTGTATGG	1646
Qy	1857	AGATGACAGAGTCTGATGGGCGAGAACAAAGTGAATTTCCAGCAGCAGCTTACCTTGTTC	1916
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Qy	1917	AAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTTCCGATTCATTCTCTGCC	1976
Db	1707	AAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTTCCGATTCATTCTCTGCC	1766
Qy	1977	CCAAGTGTGAGAGGTTCTCCCTGACATAGACAGCTTACAGATTACGATGATGATGCA	2036
Db	1767	CCAAGTGTGAGAGGTTCTCCCTGACATAGACAGCTTACAGATTACGATGATGATGCA	1826
Qy	2037	TCATTTAAGTGTGATCTAT	2056
Db	1827	TCATTTAAGTGTGATCTAT	1846

RESULT 4			
LOCUS	CR859573	3265 bp	mRNA
DEFINITION	Pongo pygmaeus mRNA; cdna DKFp459A134 (from clone DKFp459A134).		linear
ACCESSION	CR859573		
VERSION	CR859573.1	GI:55730023	
KEYWORDS	HTC.		
SOURCE	Pongo pygmaeus (orangutan)		
ORGANISM	Pongo pygmaeus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Pongo.		
REFERENCE	1 (bases 1 to 3265)		
AUTHORS	Ansoerge, W., Krieger, S., Regiert, T., Rittmueller, C., Schwager, B., Wewes, H., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.		
CONSRM	The German cdna Consortium		
TITLE	Submitted (12-NOV-2004)		
JOURNAL	MIPS, Ingolstaedter Landstr.1, D-85764		
COMMENT	Neuberberg, GERMANY		
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories,		

Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.  
 This clone (DKFZp459A134) is available at the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in Berlin, Germany.  
 Please contact RZPD for ordering:  
<http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneID=DKFZp459A134>  
 Further information about the clone and the sequencing project is available at <http://mips.gsf.de/projects/cdna/>.

## FEATURES

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## ORIGIN

Query Match 68.7%; Score 1426.2; DB 6; Length 3265;  
 Best Local Similarity 90.0%; Pred. No. 0;  
 Matches 1603; Conservative 0; Mismatches 28; Indels 150; Gaps 1;  
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 DB 292 CCCCAGGAGAGCTGCTGCAGCAGATGAAGAGCTCTGACCTGAGAACCAACGAGTGAAG 351  
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 QY 1137 CCACAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTG 1196  
 DB 1012 CCACAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGAAAGGCCCTTGGAGACTGTTG 1071  
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 DB 1072 GAAGCGAAGTGAAGACACTGAACCTCCAGGTGCACATCTCTGTTTAAGGAGCTTCAAGAGG 1131  
 QY 1257 CTCATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAAGTGTCAAG 1316  
 DB 1132 CTCATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGA- 1180  
 QY 1317 CCCTTGAAGGAAATAATTCTGCAATTCATCAGATTGATGAAAGCAAGAGCTTGT 1376  
 DB 1181 - 1180  
 QY 1377 ATACTACAAAAGTTAGAGCTACAAGTGGAAAGCATCTATCAGAAAAATCAAAATGGAAC 1436  
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 QY 1437 AGGCTAAACACAGAGGATGAAAGTCCAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1496  
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 QY 1497 TTCTTTCAGAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1556  
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 DB 1462 ATGCTGAAAGACGACGAGAGAGAAATTCATGAGCAAAAGGAGCAACTGGCAATTGCAGC 1521  
 QY 1797 TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTCGAGACCGGAGGAGGAGCTTCTGATGG 1856



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Db 1201 AATAATGCATTGAAAACAATTGAGGAACCTAACAGAAAAGAGTCAAGAAAAGTGGACAGG 1260
QY 1571 CGAGTCTCAAGGAAGTGAAGTCAAAACCTGGAACTGGCAGAGAAAGCTCTGGCTTCCAAA 1630
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QY 1631 CAGCTGCAAAATGCATGAATGAAGCAAAACCATTTGCCAGCGAAGAGAGGACCTCGAAAACC 1690
Db 1321 CAGCTGCAAAATGCATGAATGAAGCAAAACCATTTGCCAGCGAAGAGAGGACCTCGAAAACC 1380
QY 1691 ATGACATCTCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGCTGAAGAGACA 1750
Db 1381 ATGACATCTCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATGCTGAAGAGACA 1440
QY 1751 GCGAGAGAGAAATTCATGAGAGAAAGGACCACTGGCAATTCAGCTGGCAGTTCTGCTG 1810
Db 1441 GCGAGAGAGAAATTCATGAGAGAAAGGACCACTGGCAATTCAGCTGGCAGTTCTGCTG 1500
QY 1811 AAAGAGAATGATGCTTTCCAGACGCGAGCGAGCTCCTTGATGGAGATGCAGAGTGGT 1870
Db 1501 AAAGAGAATGATGCTTTCCAGACGCGAGCGAGCTCCTTGATGGAGATGCAGAGTGGT 1560
QY 1871 CATGGGCGAGAACAAAGTGACTCTCAACAGCAGGCTTACCTTGTTCAAAGAG 1922
Db 1561 CATGGGCGAGAACAAAGTGACTCTCAACAGCAGGCTTACCTTGTTCAAAGAG 1612
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## RESULT 6

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BX384735/c
LOCUS
DEFINITION
  BX384735 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
ACCESSION
  BX384735
VERSION
  BX384735.2 GI:46573611
KEYWORDS
  EST.
SOURCE
  Homo sapiens
  Homo sapiens (human)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Homnidae; Homo.
REFERENCE
  1. (bases 1 to 1089)
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
COMMENT
  On May 8, 2003 this sequence version replaced gi:30449275.
  Contact: Genoscope
  Genoscope - Centre National de Sequencage
  2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
  Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  5584.f
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?c=CS0DL001BE06NP1&c=5584.f.
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## FEATURES

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    /cell_line="RAMOS CELL LINE"
    /clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
    25-NORMALIZED"
    /note="1st strand cDNA was primed with a NotI-oligo(dT)
    primer. Five prime end enriched, double-strand cDNA was
    digested with Not I and cloned into the Not I and EcoR V
    sites of the pCMVSPORT 6 vector. Library was normalized."
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## ORIGIN

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Query Match 47.5%; Score 986.6; DB 4; Length 1089;
Best Local Similarity 96.1%; Pred. No. 5,1e-244;
Matches 1016; Conservative 14; Mismatches 24; Indels 3; Gaps 2;
QY 1014 AGCTCTCTCTGTGCTAAGGGAAGGAATCAGAAAGTGGAGAGACTTGAAGTTGCACCTCA 1073
Db 1054 ACCCGCYCTCTGTCTTCTAGGGARGGAATCAGAAGGTG--ARAAAATCTGAAGTGCACCTCA 997
QY 1074 AGGAGGCCAAGAAGAGCTTTTCAGATTTTGAAGAGAAAACACAGTAATCGTTCTTGAGATTG 1133
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QY 1134 AAACCCACAGACAGAGGGGAGACAGAGAAAGAGAAATGATGAAGAGAAAAGCCCGGAGACTG 1193
Db 936 AAACCCACAGACAGAGGGGAGACAGAGAAAGAGAAATGATGAAGAGAAAAGCCCGGAGACTG 877
QY 1194 TTGGAAGCGAAGTGAAGACACTGAACCTCCAGGTGCACATCTCTGTTTAAAGAGCTTCAAG 1253
Db 876 TTGGAAGCGAAGTGAAGACACTGAACCTCCAGGTGCACATCTCTGTTTAAAGAGCTTCAAG 817
QY 1254 AGGCTCATCAAAACTCAGCGAAGCTGAGCTTAATCAAGAGAGACTTCAAGAAAAGTGC 1313
Db 816 AGGCTCATCAAAACTCAGCGAAGCTGAGCTTAATCAAGAGAGACTTCAAGAAAAGTGC 757
QY 1314 AGGCCCTTGAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAAGCAAGAGCTTGG 1373
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QY 1374 TTTATATCAAAAGTTAGAGCTTACAAGTGGAAAAGCATGCTATCAGAAAATCAAAATGG 1433
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QY 1614 AGGCTCTGCTTCCAAACAGCTGCAAAATGGATGAATGAAGCAAAACCATTTGCCAAGCAGG 1673
Db 456 AGGCTCTGCTTCCAAACAGCTGCAAAATGGATGAATGAAGCAAAACCATTTGCCAAGCAGG 397
QY 1674 AAGAGGACCTGGAAACCACTGACCATCTCCAGGGCTCAGATGGAAGTTTACTGTTCTGTATT 1733
Db 396 AAGAGGACCTGGAAACCACTGACCATCTCCAGGGCTCAGATGGAAGTTTACTGTTCTGTATT 337
QY 1734 TTCTGCTGAAAGACAGCGAGAGAGAAAATTCATGAGAAAAGAGCAACTGGCAATTGC 1793
Db 336 TTCTGCTGAAAGACAGCGAGAGAGAAAATTCATGAGAAAAGAGCAACTGGCAATTGC 277
QY 1794 AGCTGGCAGTTCTGCTGAAAGAGAAATGATGCTTTCCGAAGACGAGCGAGCGAGTCCCTTGA 1853
Db 276 AGCTGGCAGTTCTGCTGAAAGAGAAATGATGCTTTCCGAAGACGAGCGAGCGAGTCCCTTGA 217
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QY 1914 TTCAAGAGGAGCTGAGGACAGGGGACTGGCGGCAACAGCGGAATATTTCGATTTCATCTCT 1973
Db 156 TTCAAGAGGAGCTGAGGACAGGGTACTGGCGGCAACAGCGGAATATTTCGATTTCATCTCT 97
QY 1974 GCCCAAGTGTGGAGAGGTTCTGCTGATACATAGACAGTTTACAGATTTCACGTGATGGATT 2033
Db 96 GCCCAAGTGTGGAGAGGTTCTGCTGATACATAGACAGTTTACAGATTTCACGTGATGGATT 37
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QY 2034 GCATCATTTAAGTGTGATGATATACACCTCCCAAAAC 2070
Db |||||
36 GCATCATTTAAGTGTGATGT-TCACCTCCCAAAAC 1

RESULT 7
AL583163/c
LOCUS AL583163 1068 bp mRNA linear EST 07-APR-2004
DEFINITION AL583163 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL009YF13 3-PRIME, mRNA sequence.
ACCESSION AL583163
VERSION AL583163.2 GI:31321374
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1068)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:12951861.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Creneau, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5584.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DL009CC07NP1&c=5584.f.
FEATURES
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/db_xref="taxon:9606"
/clone="CS0DL009YF13"
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/clone_lib="Homo sapiens B CELLS (RAMOS CELL LINE) COT
25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 47.3%; Score 982.6; DB 1; Length 1068;
Best Local Similarity 97.9%; Pred.No. 5.6e-243;
Matches 1019; Conservative 7; Mismatches 11; Indels 4; Gaps 3;

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1041 TTAAYTGTAGCCGCTCTGCTGTGCTTAAGGAGGGGATCAGAAAGTGGAGAGACTT 982
QY 1061 GAAGTTGC--ACTCAGGAGGCCAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTA 1118
Db |||||
981 GAAAGTGCCACTCCAAAGGAGSCCAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTA 922
QY 1119 ATCGTTCTGAGATTGAACCCACAGAGGGGAGCAGAGAAAGATGATGAGAGA 1178
Db |||||
921 ATCGTTCTGAGATTGAACCCACAGAGGGGAGMACAGAGAAAGATGATGAGAGA 862
QY 1179 AAGCCCGGAGACTGTTGAAGCCCAAGTGAACCTCCAGGTGACATCTCTGT 1238
Db |||||
861 AAGCCCGGAGACTGTTGAAGCCCAAGTGAACCTCCAGGTGAAAWCTCTGT 802
QY 1239 TTAAGGAGCTTCAAGAGGCTCATAC-AAACCTCAGCGAAGCTCAGCTTAATGAAGAGAGA 1297
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Db 801 TTAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGA 742
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741 CTTCAAGAAAGTGTTCAGGCCCTTGAAGGAAAAATTTCTCAATTCCTCATCAGAGTTCAAT 682
QY 1358 GAAAGCAAGAGCTTGTATTACTAAACAAAAGTTTAGAGCTACAAGTGGAAAAAGCATGCTA 1417
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681 GAAAGCAAGAGCTTGTATTACTAAACAAAAGTTTAGAGCTACAAGTGGAAAAAGCATGCTA 622
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621 TCAGAAATCAAAATGGAACAGAGCTTAAACACAGAGGATGAAAGTCCAAATTAACCTGTCTA 562
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QY 1718 GTTACTGTTCTGATTTTCAATGCTGAAAGAGCAGCAGAGAGAGAAAAATTCATGAGGAAAG 1777
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321 GTTACTGTTCTGATTTTCAATGCTGAAAGAGCAGCAGAGAGAGAAAAATTCATGAGGAAAG 262
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QY 1838 GGCAGGACAGTCCCTTGATGAGATGCGAGTCTGTTGGGGCGAGAACAAAGTCACTCTGAC 1897
Db |||||
201 GGCAGGACAGTCCCTTGATGAGATGCGAGTCTGTTGGGGCGAGAACAAAGTCACTCTGAC 142
QY 1898 CAGCAGGCTTACCTTCTTCAAGAGAGAGCTGAGGACAGGGAAGTGGCGGCAACAGCGGAAT 1957
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141 CAGCAGGCTTACCTTCTTCAAGAGAGAGCTGAGGACAGGGAAGTGGCGGCAACAGCGGAAT 82
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81 ATTCCGATTCATCTCTGCCCCAAGTGTGAGAGGTTCTGCTGACATAGACAGTTTACAG 22
QY 2018 ATTCCAGCTGATGATTGTCATC 2038
Db |||||
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RESULT 8
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LOCUS AL570028 1032 bp mRNA linear EST 05-APR-2004
DEFINITION AL570028 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0D1003YG24 3-PRIME, mRNA sequence.
ACCESSION AL570028
VERSION AL570028.3 GI:46236271
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 1032)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31291459.

```

Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Creteau, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five primer  
end enriched, double-strand cDNA was digested with Not I and cloned  
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library  
was normalized. Library was constructed by Life Technologies, a  
division of Invitrogen. This sequence belongs to sequence cluster  
5584.f  
For more information about this cluster, see  
<http://www.genoscope.cns.fr/cdna?s=CS0DI003BD12NP1&c=5584.f>.

FEATURES source

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1. .1032
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1003YG24"
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## ORIGIN

Query Match	46.1%;	Score 957.6;	DB 1;	Length 1032;
Best Local Similarity	95.6%;	Pred. No. 1.7e-236;		
Matches 978: Conservative	14;	Mismatches 30;	Indels 1;	Gaps 1;

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1023	Db		:
1095	Qy	CAGATTTTGAAGAAAACAAGTAATCGTTCCTGAGATTTGAAACCCAGACAGAGGGAGCA	1154
963	Db		:
1155	Qy	CAGAAAAGAGAATGATGAAGAGAAAAGCCCGGAGACTGTTTGGAAAGCGAAGTGAAGCAC	1214
903	Db		:
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783	Db		:
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723	Db		:
1395	Qy	AGCTCAAGTGGAAGCATGCTATCAGAAATCAAATGGACAGGCTAAACACAGAGNTG	1454
663	Db		:
1455	Qy	AAAAAGTCCAAATTAACCTGTGCTACAGATGACACACAAGAGCTTCTTCAAGAAATATA	1514
603	Db		:
1515	Qy	ATGCATTTGAAAACAATTTAGGAACCTAACAGAAAAGAGTCAGAAAAAGTTGACACGGGCG	1574
543	Db		:
1575	Qy	TGCTGAAGGAACTGAGTGAAAACTGGAACCTGGCAGAGAGGCTCTGGCTTCCAAAAAGC	1634
483	Db		:
1635	Qy	TGCAAAATGGATGAAATGAAGCAAAACCAATTCGCAAGCGAAGAGGAACTCGAAAAACATGA	1694
423	Db		:

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Best Local Similarity	97.4%;	Pred. No. 3.2e-231;			
Matches	963;	Conservative 5;	Mismatches 19;	Indels 2;	Gaps 2;
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Qy	1134	AAACCCACAGAGGGGAGCACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGAGACTG	1193		
Db	933	AAACCCARACAGA-GGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCGAAACTG	875		
Qy	1194	TTGAAGCGAGTGGAGCACTGAACCTCCAGGTGACATCTCTTTAAAGAGCTTCAAG	1253		
Db	874	TTGAGCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTTTAAAGAGCTTCAAG	815		
Qy	1254	AGGCTCATACAAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAGAAAGTGTC	1313		
Db	814	AGGCTCATACAAAACCTCGCGAGCTGAGCTAATGAAGAGAGACTTCAAGAGAAAGTGTC	755		
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Db	754	AGGCCCTTGAAGAGAAAATTTGCAATTCATCAGAGTTGAATGAAGAGAGAGCTTG	695		
Qy	1374	TTTATACTAAACAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAATGG	1433		
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Db	634	AACAGGCTAAACACAGAGGATGAAAGTCCAAATTAACGTCTACAGATGACACACAACA	575		
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Db	574	AGCTTCTTCAAGACATAAATAATGCATTTGAAACAAATTAGGAACTAACAGAAAGAGT	515		
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Db	514	CAGAAAAGTGGACAGGCGAGTGTCTGAAGCACTGAGTGAAGAACTGGAACCTGCGAGAGA	455		
Qy	1614	AGGCTCTGGCTTCCAAACAGCTGCAATGATGAATGAAGCAAAACCAATTCGCAAGCAGG	1673		
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Qy	1734	TTCATGCTGAAAGACGACGAGAGAGAAAATTCATGAGGAAAGAGGACCACTGCGATTGC	1793		
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Qy	1854	TGGAGTGCAGAGTCTGATGGGCGAGAACAGTGAATCTTGACCGAGGCTTACCTTG	1913		
Db	214	TGGAGTGCAGAGTCTGATGGGCGAGAACAGTGAATCTTGACCGAGGCTTACCTTG	155		
Qy	1914	TTCAAAGAGAGCTGAGCAGGAGCTGGCGGCAACAGCGGGAATATTTCCGATTCATTTCCT	1973		
Db	154	TTCAAAGAGAGCTGAGCAGGAGCTGGCGGCAACAGCGGGAATATTTCCGATTCATTTCCT	95		
Qy	1974	GCCTCAAGTGTGGAGAGTTTCTGCTGACATAGACACGTTTACAGATTCAGTGTGATG	2033		
Db	94	GCCTCAAGTGTGGAGAGTTTCTGCTTAAATAGACAGCTTACANATTCACGTGATGATT	35		
Qy	2034	GCATCAATTTAAGTGTGATGTATCACTTC	2062		
Db	34	GCATCAATTTAAGTGTGATGTATTCCTCCCC	6		

Db	368	GTCTAATGGCCTTGAGTCATGAGAATGAGAAATGAGGAGAGAGCTTGAAAACTAAAAAG	427
QY	657	GGAATATCAGAAAGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGCGCGAG	716
Db	428	GGAATATCAGAAAGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGCGCGAG	487
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Db	488	CGGAGCAGGAAAAAGGACCACTCAGGACCCAGGTGTGAGGCTCAAGCAGAGAGAGGCGAG	547
QY	777	ACTGTGTGGGCATCGTGTCTGAATCTGACCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG	836
Db	548	ACTGTGTGGGCATCGTGTCTGAATCTGACCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG	607
QY	837	ATTCTCTTTGTTGAAATTAGGATGGCTGAAGGAGAGAGGAGGAGGTCAGTAAAGAAATCA	896
Db	608	ATTCTCTTTGTTGAAATTAGGATGGCTGAAGGAGAGAGGAGGTCAGTAAAGAAATCA	667
QY	897	AGCATAGTCTCTGGGCCACGAGAACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGA	956
Db	668	AGCATAGTCTCTGGGCCACGAGAACAGTCTCCACTGGCAGCGCATTTGTCTAAATATAGA	727
QY	957	CGAATCTGCAGATGGGCGCAAGAAATTAATTCGAAATGAGGAGTAACTGTGAGCCAGC	1016
Db	728	CGAATCTGCAGATGGGCGCAAGAAATTAATTCGAAATGAGGAGTAACTGTGAGCCAGC	787
QY	1017	TCTCTGTGCTTAAGGAGGAGGATCAGAAAGTGGAGAGCTTGAAGTTCGACTCAAGG	1076
Db	788	TCTCTGTGCTTAAGGAGGAGGATCAGAAAGTGGAGAGCTTGAAGTTCGACTCAAGG	847
QY	1077	AGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAACTGTTCTGAGATTGAAA	1136
Db	848	AGGCCAAAGAAAGAGTTTCAGATTTTGAAGAAACAAAGTAACTGTTCTGAGATTGAAA	907
QY	1137	CCCAGACAGAGGGGACACAGAGAAAGAAATGATGAAGAGAAAGCCCGGAGAGCTGTG	1196
Db	908	CCCAGACAGAGGGGACACAGAGAAAGAAATGATGAAGAGAAAGCCCGGAGAGCTGTG	967
QY	1197	GAAGCGA 1203	
Db	968	GAAGCGA 974	

RESULT 11  
LOCUS BX343673/c  
DEFINITION BX343673 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI009YB18 3-PRIME, mRNA sequence.  
ACCESSION BX343673  
VERSION BX343673.2 GI:46283489  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1012)  
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
On May 2, 2003 this sequence version replaced gi:30347281.  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5584.f  
For more information about this cluster, see  
http://www.genoscope.cns.fr/cdna?s=CSIAI003B10NP1&c=5584.f.

FEATURES	Location/Qualifiers	
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	/tissue="PLACENTA COT 25-NORMALIZED"	
	/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	
	/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN		
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	Best Local Similarity 92.4%; Pred. No. 5.2e-217;	
	Matches 905; Conservative 27; Mismatches 45; Indels 2; Gaps 2;	
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Db	977	AAAGAGGKTTTCMGATTTTGAAGAAACAAADTATBTTKCTGARATK-AAACCCAGACAG 919
QY	1146	AGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTTGAAGCGAAG 1205
Db	918	A-GGGRGCACAGAGAAAGAGATGATGAAGAGAAAGSSSSGAGACTGTTTGAAGCGAAG 860
QY	1206	TGGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAA 1265
Db	859	TGGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAA 800
QY	1266	AACTCAGCGAAGCTGAGCTAATGAAGAGAGAGACTTCAAGAAAGTGTTCAGGCGCTTGA 1325
Db	799	AACTCRSGAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGTTCAGGCGCTTGA 740
QY	1326	GGAAAAATTCGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTTTATCTAAACA 1385
Db	739	GGAAAAATTCGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTTTATCTAAACA 680
QY	1386	AAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAA 1445
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Db	619	CAGAGGATGAAAAAGTCCAAATTTAACTGTGCTACAGATGACACACAAAGCTTCTTCAAG 560
QY	1506	AACATAATATGCAATTTGAAAAACAATGAGGAACTAACAGAAAGAGTCAGAAAAAGTGG 1565
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QY	1566	ACAGGGCAGTGTGAAAGGAACCTGAGTGAAGAACTGGAACCTGGCAGAGAGGCTCTGGCTT 1625
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QY	1746	GAGCAGCAGAGAGAGAAAAATTCATGAGGAAAAAGGAGCAACTGGCATTGCAAGTGGCAGTTTC 1805
Db	319	GAGCAGCAGAGAGAGAAAAATTCATGAGGAAAAAGGAGCAACTGGCATTGCAAGTGGCAGTTTC 260
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Db	259	TGCTGAAAGAGAAATCATGCTTTTCGAAGACGGAGGAGGAGGCTCTTGTATGGAGATCGAGA 200
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Db 239 CCCCGAGGAGCTCTGTCAGCAGATGAAAGAGCTCTTGACCAAGAACCAACAGCTGAAAG 298
Qy 477 AAGCCATGAGCTAAATCAAGCCATGAAGGAGATTTGAGGAGCTTTCGGCTTGA 536
Db 299 AAGCCATGAGCTAAATCAAGCCATGAAGGAGATTTGAGGAGCTTTCGGCTTGA 358
Qy 537 CAGAGAAACAGAGGAAGAACGCCAGTGTGATGATACAGACCAAGAGCAAAAGAGC 596
Db 359 CAGAGAAACAGAGGAAGAACGCCAGTGTGATGATACAGACCAAGAGCAAAAGAGC 418
Qy 597 GTCTAATGGCTTGAAGTATGAGAAATGAGAAATGAGAAAGAGCTTGGAAAACATAAAG 656
Db 419 GTCTAATGGCTTGAAGTATGAGAAATGAGAAATGAGAAAGAGCTTGGAAAACATAAAG 478
Qy 657 GGAATCAGAAAGTCTATCTGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG 716
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Qy 717 CGAGACAGGAAAGGACAGCTCAGGACCCAGAGTGGTGAGGCTCAACAGCAGAGAGGCAG 776
Db 539 CGAGACAGGAAAGGACAGCTCAGGACCCAGAGTGGTGAGGCTCAACAGCAGAGAGGCAG 598
Qy 777 ACTGTGGGATCGTGTCTGAACTGAGCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG 836
Db 599 ACTGTGGGATCGTGTCTGAACTGAGCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG 658
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Db 659 ATTCTTTGTGTAATTAGATGCTGAGGAGGAGCAGAGAGGCTGAGTAAAGAAATCA 718
Qy 897 AGCATAGTCTGGGCCCAAGCAAGTCTCCACTGGCAGCGCATCTGCTAAATATAGGA 956
Db 719 AGCATAGTCTGGGCCCAAGCAAGTCTCCACTGGCAGCGCATCTGCTAAATATAGGA 778
Qy 957 GCAGATCTGAGATGGGGCCCAAGAAATTAATTCGAACATGAGGAGTAACTGTGAGCCAGC 1016
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Qy 1017 TCCTGCTGCTTAAGGGAAGGAGATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGG 1076
Db 839 TCCTGCTGCTTAAGGGAAGGAGATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGG 898
Qy 1077 AGGCCAAAGAAAGATTTTCAGATTTTGAAGAAACAAAGTAACTGCTGAGATTGAAA 1136
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Db 957 -CCAGACAGAGGGGAGCAC--AAGAAAGAGATGATGAAGAAAGGCC 1001
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RESULT 15
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LOCUS
DEFINITION Pan troglodytes OPTN gene, VIRUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION DQ036022
VERSION DQ036022.1
KEYWORDS GI:66887231
SOURCE GSS.
ORGANISM Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Pan.
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REFERENCE 1 (bases 1 to 1497)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE A Scan for Positively Selected Genes in the Genomes of Humans and
Chimpanzees
JOURNAL (er) PLOS Biol. 3 (6), E170 (2005)
PUBMED 15869325
REFERENCE 2 (bases 1 to 1497)
AUTHORS Nielsen,R., Bustamante,C., Clark,A.G., Glanowski,S., Sackton,T.B.,
Hubisz,M.J., Fiedel-Alon,A., Tanenbaum,D.M., Civallo,D.,
White,T.J., Shinsky,J.J., Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (05-MAY-2005) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment. Translation starts at the beginning of
alignment.
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/mol_type="genomic DNA"
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gene <1..51497
/genes="OPTN"
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Best Local Similarity 55.3%; Pred. No. 6.4e-202;
Matches 828; Conservative 0; Mismatches 669; Indels 0; Gaps 0;
Qy 341 GAAAAGGAGGACAGCCCCAGTGAAAGCACAGGAAATGGACCCCACTGGCCACCCCA 400
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Qy 401 AACCTGGACAGCTTTACCCGGAGGAGCTGCTGCAGCAGATGAAAGAGCTCTTGACCAAG 460
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Qy 521 GAGCTTTGGCCCTGGACAGAGAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 580
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Qy 701 CTTCCCAAGGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 760
Db 361 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 420
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Db 421 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480
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Db 481 AGCGGCTCTCAGAGAGATTCCTTTGTTGAAATTTAGGATGGCTGAAAGAGGAGGAGGAGG 540
Qy 881 TCAGTAAAGAAATCAAGCATAGTCTGGGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 940
Db 541 TCAGTAAAGAAATCAAGCATAGTCTGGGCCCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 600
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Db 661 CTCAGCTGAATCTCAGCGGCTCTCAGAGATTCCTTTGTTGAAATGAGATGGCTGAA 720
Qy 866 GGAGAGCAGAGGCTCAGTAAAGAAATCAGCATAGTCTGGGCCCCAGAGACAGTC 925
Db 721 GGAGAGCAGAGGCTCAGTAAAGAAATCAGCATAGTCTGGGCCCCAGAGACAGTC 780
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Db 781 TCCACTGGCAGCGCATTTGCTAAATATAGG 810

RESULT 17
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LOCUS AL565248 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
DEFINITION CS0DP002YP13 3-PRIME, mRNA sequence.
ACCESSION AL565248
VERSION AL565248.3 GI:46232132
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 882)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:30549100.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5584.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DP002CH07NP1&c=5584.f.
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Best Local Similarity 94.2%; Pred. No. 1.2e-195;
Matches 821; Conservative 15; Mismatches 35; Indels 1; Gaps 1;

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Qy 1384 CAAAAAGTTAGAGCTCAAGTGGAAGAGCTGCTATCAGAAATCAAAATGAAACAGGCTAA 1443
Db 698 CAAAAAGTTAGAGCTCAAGTGGAAGAGCTGCTATCAGAAATCAAAATGGAACAGGCTAA 639
Qy 1444 AACAGAGGATGAAAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGCTTTCTCA 1503
Db 638 AACAGAGGATGAAAAAGTCCAAATTAATCTGTCTACAGATGACACACAAAGCTTTCTCA 579
Qy 1504 AGAACAATAATATGCAATTTGAAAACAATTTAGGAACTAAACAAAGAAAGAGTCAGAAAAGT 1563
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Qy 1624 TTCCAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAGGAAGAGACCT 1683
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Qy 1684 GGAACCATGACCATCTCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTGCTGA 1743
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Db 218 GAGTCCTCATGAGGGCGAGAAACAAGTCACTCTGACAGCAGGCTTACTGTTTCAAGAGG 159
Qy 1924 AGCTGAGGACAGGACTGGGCGCAACAGCGGATATTCGATTCATTCTCTGCCCAAGTG 1983
Db 158 AGCTGAGGACAGGACTGGGCGCAACAGCGGATATTCGATTCATTCTCTGCCCAAGTG 99
Qy 1984 TGGAGAGGTTCTGCTCTGACATAGACAGCTTACAGATTCACGTGATGATGCATCATTTA 2043
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Db 38 AGTGTGAT-TATCACTCCCSVAAAACCTGTTG 8

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/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
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RESULT 18
AL516922      955 bp      mRNA      linear      EST 23-MAR-2004
LOCUS        Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION   CSODA007YM21 5-PRIME, mRNA sequence.
ACCESSION    AL516922
VERSION      AL516922.3 GI:456533531
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 955)
AUTHORS      Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE        Full-length cDNA libraries and normalization
JOURNAL      Unpublished (2001)
COMMENT      On Feb 13, 2001 this sequence version replaced gi:30492030.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo (dr) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
              was not normalized. Library was constructed by Life Technologies, a
              division of Invitrogen.
              This sequence belongs to sequence cluster 5584.f
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?s=CSODA007AG11QP1&c=5584.f.
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                  /note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
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                  the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                  Library was not normalized."
ORIGIN
Query Match      38.4%; Score 797; DB 1; Length 955;
Best Local Similarity 93.1%; Pred. No. 7.1e-195;
Matches 817; Conservative 31; Mismatches 27; Indels 3; Gaps 2;
QY 297 CAGGAACCTTCGAATGTCGATCCGATCACTCTCAGCTGCTCCTCACTGAAAGGAGGACGCC 356
DB 79 CAGGAACCTTCGAAATGTCGATCCGATCACTCTCAGCTGCTCCTCACTGAAAGGAGGACGCC 138
QY 357 CCAGTGAAGAGCAGAGAAATGACCCGCCACCTGGCCACCCACCAACCTGGACAGCTTTA 416
DB 139 CCAGTGAAGAGCAGAGAAATGACCCGCCACCTGGCCACCCACCAACCTGGACAGCTTTA 198
QY 417 CCCCAGAGAGCTGCTGACGAGATGAAGAGCTCCTGACCAAGAACCAACAGCTGAAAG 476
DB 199 CCCCAGAGAGCTGCTGACGAGATGAAGAGCTCCTGACCCAGAACCAACAGCTGAAAG 258
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QY 537 CAGAGAAACAGAGGAGAAACGCCAGTTTTTTTGGAGATACAGAGCAAGAAAGCAAAAGAGC 596
DB 319 CAGAGAAACAGAGGAGAAACGCCAGTTTTTTTGGAGATACAGAGCAAGAAAGCAAAAGAGC 378
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Db 379 GTCTAATGCGCTTGAGTTATGAGAAATKAGAGAAAGAGCTTGAAAACTAAAG 438
QY 657 GGAATCAGAAAGCTCATCTCAGGACCCCACTGATGACTCCAGGCTTCCCAGGCGGAG 716
DB 439 GGAATCAGAAAGGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCCAGGCGGAG 498
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QY 777 ACCTGTTGGGCATCGTGTCTGAACTGAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAG 836
DB 559 ANCTGTTGGGCATCGTGTCTGAACTGAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAG 618
QY 837 ATTCCTTTGTTGAAATTAGGATGGCTGAAGAGAGCAGAGAGGGTTCAGTAAAGAAATCA 896
DB 619 ATTCCTTTGTTGATATTAGGATGGCTGAAGAGAGCAGAGAGGGTTCAGTAAAGAAATCA 678
QY 897 AGCATAGTCTCTGGGCCACGAGACAGTCTCCACTGGCACGGCATTTGTCTAAATATAGGA 956
DB 679 AGCATAGTCTCTGGGCCACGAGACAGTCTWCACCTGGCACGGCATTTGTAAATATAGGA 738
QY 957 GCAGATCTGAGATGGGGCCAAAGAAATTACTTCGAAACATGAGAGTTAACTGTGAGCCAGC 1016
DB 739 GCAGATCTGAGATGGGGCCAAAGAAATTACTTCGAAACATGAGAGTTAACTGTGAGCCAGC 798
QY 1017 TCCTGCTGCTGAAGGAGGAGATCAGAGGTGGAGAGCTTGAAGTTGCACCTCAAGG 1076
DB 799 CACTGCTGTGCTWAGGAGGAGGATCAGAGGTGGAGARA-YTKAAGTTTTCACCTCAAGG 857
QY 1077 AGGCCAAAGAAAGAGTTTTCAGATTTTGAAAGAAAAACAAGTAATCGTTCTGAGATTGAAA 1136
DB 858 AGGSCMAAGAAAGAGTTTTCAGATTTTTAAARAAARAAARAA--TAACTTCTKARATTAAA 915
QY 1137 CCCAGACAGAGGGGACGACAGAGAAAGAGAAATGATGAA 1174
DB 916 CWRARAGAGGGGCGMRERAGAAARAKAATAATKARMAAA 953
RESULT 19
BU161830      882 bp      mRNA      linear      EST 04-SEP-2002
LOCUS        AGENCOURT 7967200 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6162276
DEFINITION   5', mRNA sequence.
ACCESSION    BU161830
VERSION      BU161830.1 GI:22675740
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 882)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE        National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
              Email: cgapbs-remail.nih.gov
              Tissue Procurement: ATCC/DCTD/DTF
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
              DNA Sequencing by: Agencourt Bioscience Corporation
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM13515 row: o column: 13
              High quality sequence stop: 699.
              Location/Qualifiers
                  1..882
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                      /mol_type="mRNA"
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                      /clone="IMAGE:6162276"
FEATURES     source
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/tissue\_type="melanotic melanoma"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_72"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1; NotI;  
Site 2; SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 2 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 38.0%; Score 789.2; DB 3; Length 882;  
Best Local Similarity 97.5%; Pred. No. 7.3e-193;  
Matches 811; Conservative 0; Mismatches 20; Indels 1; Gaps 1;  
QY 759 TACAAGCAGAGAAGCGACAGCTGTGGGCATCGTGTCTGAACCTCAAGCTGAACCT 818  
Db 1 TACAAGCAGAGAAGCGACAGCTGTGGGCATCGTGTCTGAACCTCAAGCTGAACCT 60  
QY 819 CCAGCGCTCTCAGAGATCTCTTCTGAATTAGGATGGCTGAAGGAGACAGAG 878  
Db 61 CCAGCGCTCTCAGAGATCTCTTCTGAATTAGGATGGCTGAAGGAGACAGAG 120  
QY 879 GGTCAAGTAAAGAAATCAAGCATAGTCTCTGGGCCACGAGAACAGTCTCCACTGGCACGG 938  
Db 121 GGTCAAGTAAAGAAATCAAGCATAGTCTCTGGGCCACGAGAACAGTCTCCACTGGCACGG 180  
QY 939 CATGTCTAAATATAGGAGCAGATCTGCAGATGGGGCCAAAGAAATTAATTCGAACATGAGG 998  
Db 181 CATGTCTAAATATAGGAGCAGATCTGCAGATGGGGCCAAAGAAATTAATTCGAACATGAGG 240  
QY 999 AGTTAACTGTAGCCAGCTCTCTGTGCTTGAAGGAGGAAATCAAGAGTGGAGAGAC 1058  
Db 241 AGTTAACTGTAGCCAGCTCTCTGTGCTTGAAGGAGGAAATCAAGAGTGGAGAGAC 300  
QY 1059 TTCAAGTTGACCTCAAGAGGCGCAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAGTA 1118  
Db 301 TTCAAGTTGACCTCAAGAGGCGCAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAGTA 360  
QY 1119 ATCGTTCTGAGATTGAACCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGA 1178  
Db 361 ATCGTTCTGAGATTGAACCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAAGAGA 420  
QY 1179 AAGCCCGAGAGCTGTGGAAGCGAAGTGAAGCAGTGAACCTCCAGGTGACATCTCTGT 1238  
Db 421 AAGCCCGAGAGCTGTGGAAGCGAAGTGAAGCAGTGAACCTCCAGGTGACATCTCTGT 480  
QY 1239 TTAAGGAGCTTCAAGAGCTCATACAAACTCAGCGAAGCTGAGCTAATGAAGAGAGAC 1298  
Db 481 TTAAGGAGCTTCAAGAGCTCATACAAACTCAGCGAAGCTGAGCTAATGAAGAGAGAC 540  
QY 1299 TTCAAGAAAGTGTCAAGGCCCTTTGAAGGAAAGAAATTCGCAATTTCCATCAGAGTTGAATG 1358  
Db 541 TTCAAGAAAGTGTCAAGGCCCTTTGAAGGAAAGAAATTCGCAATTTCCATCAGAGTTGAATG 600  
QY 1359 AAAAGCAGAGCTGTGTTATCTAAACAAAGTTAGAGCTTACAGTGGAAAGCATGCTAT 1418  
Db 601 AAAAGCAGAGCTGTGTTATCTAAACAAAGTTAGAGCTTACAGTGGAAAGCATGCTAT 660  
QY 1419 CAGAAATCAAAATGGAACAGGCTTAAACAGAGATGAAGAGTCCAAATTAATCTGCTAC 1478  
Db 661 CAGAAATCAAAATGGAACAGGCTTAAACAGAGATGAAGAGTCCAAATTAATCTGCTAC 720  
QY 1479 AGATGACACACAAAGCTTCTTCAAGAAACATATATATGATTTGAAACAAATTTGAGG-AA 1537  
Db 721 AGATGACACACAAAGCTTCTTCAAGAAACATATATATGATTTGAAACAAATTTGAGGAA 780  
QY 1538 CTAACAGAAAGAGTCAAGAAAGTGAACAGGCGAGTGTCTGAAGGAGCTGA 1589  
Db 781 CTAACAGAAAGAGTCCGAANAAGTGGGACAGGGCGAGTGGCTGAAGGGA 832

RESULT 20

AL543413

LOCUS

968 bp mRNA linear EST 24-MAR-2004

## DEFINITION

AL543413 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
clone CSODI003YG24 5-PRIME, mRNA sequence.

## ACCESSION

AL543413

## VERSION

AL543413.3

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 968)

## AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

## TITLE

Full-length cDNA libraries and normalization

## JOURNAL

Unpublished (2001)

## COMMENT

On Feb 15, 2001 this sequence version replaced gi:31265260.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

5584.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODI003BD12QP1&c=5584.f.

## FEATURES

Location/Qualifiers

1..968

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODI003YG24"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 37.4%; Score 777.2; DB 1; Length 968;

Best Local Similarity 94.4%; Pred. No. 9.7e-190;

Matches 829; Conservative 11; Mismatches 18; Indels 20; Gaps 3;

QY 297 CAGGAACCTTCTCAATGTCCCATCAACCTCTCAGCTCCTCACTGAAAGGAGGACAGCC 356

Db 104 CAGGAACCTTCTCAATGTCCCATCAACCTCTCAGCTCCTCACTGAAAGGAGGACAGCC 163

QY 357 CCAGTGAAGACAGAGAAATGGACCCCTGCGCCACCCCAACCTGGACACCGTTTA 416

Db 164 CCAGTGAAGACAGAGAAATGGACCCCTGCGCCACCCCAACCTGGACACCGTTTA 223

QY 417 CCCCAGGAGCTGCTGCAGCAGATGAAAGAGCTCTGACCAAGAAACCCACCTGAAAG 476

Db 224 CCCCAGGAGCTGCTGCAGCAGATGAAAGAGCTCTGACCAAGAAACCCACCTGAAAG 283

QY 477 AAGCCATGAGCTTAATATCAAGCCATGAAGGGAGATTTGAGGAGCTTTCGGCTGGA 536

Db 284 AAGCCATGAGCTTAATATCAAGCCATGAAGGGAGATTTGAGGAGCTTTCGGCTGGA 343

QY 537 CAGAGAAAACAGAGGAGAAACGCCAGTCTTTTGTAGATACAGAGCAAGAAAGCAAGAGAGC 596

Db 344 CAGAGAAAACAGAGGAGAAACGCCAGTCTTTTGTAGATACAGAGCAAGAAAGCAAGAGAGC 403

QY 597 GTCTAATGCGCTTGAGTCTATGAGAAATGAGAAATTTGAAGAAAGAGCTTGGAAACTAAAAG 656

Db 404 GTCTAATGCGCTTGAGTCTATGAGAAATTTGAAGAAAGAGCTTGGAAACTAAAAG 463

QY 657 GGAAATCAGAAAGGTCATCTGAGGAGCCCACTGATGACTCCAGGCTTCCAGAGGCCGAG 716

Db 464 GGAAATCAGAAAGGTCATCTGAGGAGCCCACTGATGACTCCAGGCTTCCAGAGGCCGAG 523



AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: James Martin  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Clone distribution information can be obtained  
from Dr. M. Bento Soares, [bento-soares@uiowa.edu](mailto:bento-soares@uiowa.edu)  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-H-FLI-bgc-g-19-0-UI"  
/tissue\_types="Cell lines"  
/dev\_stage="Adult"  
/lab\_host="DH10B (Life Technologies)"  
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/notes="Organ: Chondrosarcoma; Vector: pT73-Pac  
(Pharmacia) with a modified polylinker; Site 1: EcoR I;  
Site 2: Not I; NCI CGAP FLI is a normalized CDNA library  
derived from a pool of mRNA obtained from 4 cell lines  
from grade III chondrosarcoma tissues. The library was  
constructed according to Bonaldo, Lennon and Soares,  
Genome Research, 6:791-806, 1996. First strand cDNA  
synthesis was primed with an oligo-dT primer containing a  
Not I site. Double stranded cDNA was ligated to an EcoR I  
adaptor, digested with Not I, and cloned directionally  
into pT73-Pac vector. The oligonucleotide used to prime  
the synthesis of first-strand cDNA contains a library tag  
sequence that is located between the Not I site and the  
(dT)18 tail. The sequence tag for this library is  
GAGTCCGGTG. The cell lines were provided by Dr. James  
Martin from the University of Iowa.  
TAG\_TISSUE=Human Chondrosarcoma Grade 3 cell line mix  
TAG\_LIB=UI-H-FLI  
TAG\_SEQ=GAGGTCGGTG"

ORIGIN

Query Match 37.1%; Score 771.4; DB 3; Length 817;  
Best Local Similarity 99.6%; Pred. No. 2.9e-188;  
Matches 772; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1303 AGAAAAAGTGTGAGGCGCTTGAAGGAAAAATTCGCAATTCATCAGAGTTGAATGAAAA 1362  
DB 817 AGAAAAAGTGTGAGGCGCTTGAAGGAAAAATTCGCAATTCATCAGAGTTGAATGAAAA 758  
QY 1363 GCAAGAGCTGTTTATCTAACAAAAAGTTAGAGCTACAGTGAAGGAAAGCATGTATCAGA 1422  
DB 757 GCAAGAGCTGTTTATCTAACAAAAAGTTAGAGCTACAGTGAAGGAAAGCATGTATCAGA 698  
QY 1423 AATCAAAATGGAACAGCGCTTAACACAGGATGAAGATCCAAATTAAGTGTGCTACAGAT 1482  
DB 697 AATCAAAATGGAACAGCGCTTAACACAGGATGAAGATCCAAATTAAGTGTGCTACAGAT 638  
QY 1483 GACACACAACAGCTTCTTCAAGAACATATATGCAATGAAAAACAATTGAGGAACTAAC 1542  
DB 637 GACACACAACAGCTTCTTCAAGAACATATATGCAATGAAAAACAATTGAGGAACTAAC 578  
QY 1543 AGAAAAAGAGTCAGAAAAAGTGACAGGGCAGTGTCTGAAGGAACTGAGTGAAGAACTGGA 1602  
DB 577 AGAAAAAGAGTCAGAAAAAGTGACAGGGCAGTGTCTGAAGGAACTGAGTGAAGAACTGGA 518  
QY 1603 ACTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCAATGGATGAATGAAGCAACCAT 1662  
DB 517 ACTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCAATGGATGAATGAAGCAACCAT 458

QY 1663 TGCCAAAGCAGGAGAGGAGCACTGGAAACCATGACCATCCTCAGGGCTCAGATGGAAGTTTA 1722  
DB 457 TGCCAAAGCAGGAGAGGAGCACTGGAAACCATGACCATCCTCAGGGCTCAGATGGAAGTTTA 398  
QY 1723 CTGTTCTGATTTTCATGCTGAAAGAGCAGGAGAGAGAAAAATTCATGAGGAAAGGAGCA 1782  
DB 397 CTGTTCTGATTTTCATGCTGAAAGAGCAGGAGAGAGAAAAATTCATGAGGAAAGGAGCA 338  
QY 1783 ACTGGCATTGCAGCTGGCAGTTCCTGCTGAAAGAGAAATGATGCTTTCGAACACGGAGCAG 1842  
DB 337 ACTGGCATTGCAGCTGGCAGTTCCTGCTGAAAGAGAAATGATGCTTTCGAACACGGAGCAG 278  
QY 1843 GCAGTCCTTGTATGAGATGCAGAGTCGTATGATGGGGGAGAGCAAAAGTACTCTGACCAGCA 1902  
DB 277 GCAGTCCTTGTATGAGATGCAGAGTCGTATGATGGGGGAGAGCAAAAGTACTCTGACCAGCA 218  
QY 1903 GGCCTTACCTTGTTCAGAGAGGAGCTGAGGACAGGGAGCTGGCGGCAACAGCGGAATATTC 1962  
DB 217 GGCCTTACCTTGTTCAGAGAGGAGCTGAGGACAGGGAGCTGGCGGCAACAGCGGAATATTC 158  
QY 1963 GATTCAATTCCTGCCCCCAAGTGTGGAGAGGTTCTGCTCTGACATAGACACGTTACAGATTCA 2022  
DB 157 GATTCAATTCCTGCCCCCAAGTGTGGAGAGGTTCTGCTCTGACATAGACACGTTACAGATTCA 98  
QY 2023 CGTGATGGATTGCATCATTTAAAGTGTGATGATATCACCTCCCAAAACTGTTGGT 2077  
DB 97 CGTGATGGATTGCATCATTTAAAGTGTGATGATATCACCTCCCAAAACTGTTGGT 43  
RESULT 23  
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LOCUS 601487327F1 NIH\_MGC\_69 Homo sapiens CDNA clone IMAGE:3889542 5',  
DEFINITION mRNA sequence.  
ACCESSION BE875862  
VERSION BE875862.1 GI:10324638  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.  
REFERENCE 1 (bases 1 to 945)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP/Gazdar  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9671 row: f column: 07  
High quality sequence stop: 675.  
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/organism="Homo sapiens"  
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/clone\_lib="NIH MGC 69"  
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.1 kb. Library constructed by Life  
Technologies."  
ORIGIN  
Query Match 37.1%; Score 770; DB 7; Length 945;

Best Local Similarity 96.5%; Pred. No. 7.1e-188;			
Matches 808; Conservative 0; Mismatches 26; Indels 3; Gaps 2;			
QY	565	TTTTGAGATACAGAGCAAGAGCAAGAGCGTCTAATGGCCTTGAAGTCATGAGAATGA	624
Db	1	TTTTGAGATACAGAGCAAGAGCAAGAGCGTCTAATGGCCTTGAAGTCATGAGAATGA	60
QY	625	GAATTTGAAGGAGAGCTTGGAAAACTAAAGGGAAATCAGAAAAAGTCTATCTGAGACCC	684
Db	61	GAATTTGAAGGAGAGCTTGGAAAACTAAAGGGAAATCAGAAAAAGTCTATCTGAGACCC	120
QY	685	CACTGATGACTCCAGGCTTCCAGGGCCGAAGCGAGCAGGAGGAAAAAGCAGCTCAGGAC	744
Db	121	CACTGATGACTCCAGGCTTCCAGGGCCGAAGCGAGCAGGAGGAAAAAGCAGCTCAGGAC	180
QY	745	CCAGTGGTGAGGCTACAAGCAGAGAGAGGAGCAGACCTTTGGGCATCTGTCTGAACCTGA	804
Db	181	CCAGTGGTGAGGCTACAAGCAGAGAGAGGAGCAGACCTTTGGGCATCTGTCTGAACCTGA	240
QY	805	GCTCAAGCTGAATCTCCAGCGGCTCCTCAGAAGATTCTTTGTTGAAATTTAGGATGGCTGA	864
Db	241	GCTCAAGCTGAATCTCCAGCGGCTCCTCAGAAGATTCTTTGTTGAAATTTAGGATGGCTGA	300
QY	865	AGGAGAGCAGAGGCTCAGTAAAAAGAAATCAAGCATAGTCTCTGGGCCACAGAACAGT	924
Db	301	AGGAGAGCAGAGGCTCAGTAAAAAGAAATCAAGCATAGTCTCTGGGCCACAGAACAGT	360
QY	925	CTCCACTGCGACGGCATTGCTTAATATATAGGAGCAGATCTGAGATGGGCCCAAGAAATTA	984
Db	361	CTCCACTGCGACGGCATTGCTTAATATATAGGAGCAGATCTGAGATGGGCCCAAGAAATTA	420
QY	985	CTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCTCTGTCTGCTTAAGGGAAGGAATCA	1044
Db	421	CTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCTCTGTCTGCTTAAGGGAAGGAATCA	480
QY	1045	GAAGTGGAGAGACTTTGAAGTTGCACTCAAGGAGGCCAAAGAAAGAGTTTCAGATTTTGA	1104
Db	481	GAAGTGGAGAGACTTTGAAGTTGCACTCAAGGAGGCCAAAGAAAGAGTTTCAGATTTTGA	540
QY	1105	AAAGAAAACAAGTAATCGTTCTGAGATTGAATCCAGCAGAGAGGGAGCAGAGAAAGA	1164
Db	541	AAAGAAAACAAGTAATCGTTCTGAGATTGAATCCAGCAGAGAGGGAGCAGAGAAAGA	600
QY	1165	GAATGATGAAGAGAGAGGCCGAGACTGTTGGAAGCAAGTGAAGCACTCAACTCA	1224
Db	601	GAATGATGAAGAGAGAGGCCGAGACTGTTGGAAGCAAGTGAAGCACTCAACTCA	659
QY	1225	GGTGACATCTCTGTTTGAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGCTGAGCT	1284
Db	660	NGTGACATCTCTGTTTGAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGTTGAGTA	719
QY	1285	AATGAAGAAGAGACTTCAAGAAAAGTGTGAGGCCCTTGAAGGAAAAATTTGCAATTCC	1344
Db	720	ATGGAAGAAGAGACTTCAAGAAAAGTGTGAGGCCCTTGAAGGAAAAATTTGCAATTCC	777
QY	1345	ATCAGAGTTGAATGAAAAACAAGAGCTCTGTTTATACATAAAAAAGTTAGAGCTACA	1401
Db	778	ATCAGAGTTGAATGAAAAACAAGAGCTCTGTTTATACATAAAAAAGTTAGAGCTACA	834

RESULT 24  
CD243803  
LOCUS  
DEFINITION  
AGENCOURT\_14099182 NIH\_MGC\_180 Homo sapiens CDNA clone  
IMAGE:30377971 5', mRNA sequence.  
ACCESSION  
CD243803  
VERSION  
CD243803.1 GI:31004267  
KEYWORDS  
EST.  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo.

REFERENCE AUTHORS TITLE JOURNAL COMMENT	1 (bases 1 to 854) NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: Dr. Michael Brownstein cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDAM443 row: a column: 20 High quality sequence stop: 615.									
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	ORIGIN Query Match 36.8%; Score 763.8; DB 5; Length 854; Best Local Similarity 99.7%; Pred. No. 2.8e-186; Matches 765; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
	QY	421	GGAGGAGCTGCTGCAGCAGATGAAAGAGCTCTCTGACCAAGAACCCACAGCTGAAAGAGC	480						
	Db	1	GGAGGAGCTGCTGCAGCAGATGAAAGAGCTCTCTGACCGAGAACCCACAGCTGAAAGAGC	60						
	QY	481	CATGAAGCTAAATCAAGCCATGAAGGAGATTTGAGGAGCTTTGCGGCTGGACAGA	540						
	Db	61	CATGAAGCTAAATCAAGCCATGAAGGAGATTTGAGGAGCTTTGCGGCTGGACAGA	120						
	QY	541	GAACAGAGGAAGAACGCCAGTCTTTTGAGATACAGAGCAAGAAAGCAAGAGCGTCT	600						
	Db	121	GAACAGAGGAAGAACGCCAGTCTTTTGAGATACAGAGCAAGAAAGCAAGAGCGTCT	180						
	QY	601	AATGGCCTTGAGTCATGAGAAATGAGAAATTGAAGGAAGAGCTTGGAAAACTAAAAAGGAA	660						
Db	181	AATGGCCTTGAGTCATGAGAAATGAGAAATTGAAGGAAGAGCTTGGAAAACTAAAAAGGAA	240							
QY	661	ATCAGAAAGTCACTGAGGAGCCCACTGATGACTCCAGGCTTCCAGGGCCGAGACCGGA	720							
Db	241	ATCAGAAAGTCACTGAGGAGCCCACTGATGACTCCAGGCTTCCAGGGCCGAGACCGGA	300							
QY	721	GCAGGAAAAAGGACACAGCTCAGGACCCAGTGTGAGGCTTACAAGCAGAGAGAGCGAGCCT	780							
Db	301	GCAGGAAAAAGGACACAGCTCAGGACCCAGTGTGAGGCTTACAAGCAGAGAGAGCGAGCT	360							
QY	781	GTTGGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGGGCTCTCTCAGAAAGTTC	840							
Db	361	GTTGGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGGGCTCTCTCAGAAAGTTC	420							
QY	841	CTTTGTTGAAATTTAGGATGGCTGAAGGAGAGCAGAGGGTCAGTAAAGAAATCAAGCA	900							
Db	421	CTTTGTTGAAATTTAGGATGGCTGAAGGAGAGCAGAGGGTCAGTAAAGAAATCAAGCA	480							
QY	901	TAGTCTCGGGCCCGCAGAGAACAGTCTCCACTGGCACGGCATTTGCTTAAATATAGGAGCAG	960							
Db	481	TAGTCTCGGGCCCGCAGAGAACAGTCTCCACTGGCACGGCATTTGCTTAAATATAGGAGCAG	540							
QY	961	ATCTGCAGATGGGGCCCAAGAAATTAATCTCGAAATGAGGAGTTAACTGTGAGGACGCTCT	1020							



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Db      541 ATCTGCAGATGGGGCCAAAGAAATTACTTCGAACATGAGGAGTTAACTGTGTAGCCAGCTCCT 600
Qy      1021 GCTGTGCTTAAGGGAAGGGGAATCAGAGGTGGAGAGACTTTGAAGTTGCACTCAAGGAGGC 1080
Db      601 GCTGTGCTTAAGGGAAGGGGATCAGAGGTGGAGAGACTTTGAAGTTGCACTCAAGGAGGC 660
Qy      1081 CAAAGAAGAGTTTCAGATTTTGAAGAAGAAAAACAAGTAATCGTTCTGAGATTGAAACCCCA 1140
Db      661 CAAAGAAGAGTTTCAGATTTTGAAGAAGAAAAACAAGTAATCGTTCTGAGATTGAAACCCCA 720
Qy      1141 GACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCG 1187
Db      721 GACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCG 767

RESULT 25
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LOCUS      990 bp mRNA linear EST 08-APR-2004
DEFINITION BX364738 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI009YB18 5-PRIME, mRNA sequence.
ACCESSION BX364738
VERSION    BX364738.2 GI:46286045
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 990)
AUTHORS    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    On May 5, 2003 this sequence version replaced gi:30366842.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5584.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1A10032B10QP1k=5584.f.

FEATURES             source
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/organism="Homo sapiens"
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/clone="CSODI009YB18"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match      36.0%; Score 747.6; DB 4; Length 990;
Best Local Similarity 90.8%; Pred. No. 4.6e-182;
Matches 799; Conservative 30; Mismatches 29; Indels 22; Gaps 3;

Qy      297 CAGGAATCTTCGAATGCTCCATCACTCTCAGCTGCCTCACTGAAAGGAGGAGCC 356
Db      131 CAGGAATCTTCGAATGCTCCATCACTCTCAGCTGCCTCACTGAAAGGAGGAGCC 190
Qy      357 CCAGTGAAGACAGAGAAATGGACCCGCCACCTGGCCACCCACCAACCTGGACACGTTTA 416
Db      191 CCAGTGAAGACAGAGAAATGGACCCGCCACCTGGCCACCCACCAACCTGGACACGTTTA 250
Qy      417 CCCCAGGAGGTGCTGACAGATGAAAGAGTCTCTGACCAAGAACCCAGCTGAAAG 476

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Db      251 CCCCGAGGAGCTGTGTCAGCAGATGAAAGAGCTCCTGACCGAGAACCCAGCTGAAAG 310
Qy      477 AAGCCATGAAGCTAAATAATCAAGCCATGAAGGGGAGATTTTGAGGAGCTTTTCGGCTTGA 536
Db      311 AAGCCATGAAGCTAAATAATCAAGCCATGAAGGGGAGATTTTGAGGAGCTTTTCGGCTTGA 370
Qy      537 CAGAGAAAACAGAGGAAGAACCGCCAGTTTTTTTGTAGATACAGAGCAAGCAAAAGAGAGC 596
Db      371 CAGAGAAAACAGAGGAAGAACCGCCAGTTTTTTTGTAGATACAGAGCAAGCAAAAGAGAGC 430
Qy      597 GTCTAATGCGCTTGAGTCATGAGTAATGAGNAATTTGAGNAAGAGCTTTGNAAACTAAAG 656
Db      431 GTCTAATGCGCTTGAGTCATGAGTAATTTGAAGGAAGAGCTTTGGAATACTAAAG 490
Qy      657 GGAAATCAGAAAAGGTCTATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAG 716
Db      491 GGAAATCAGAAAAGGTCTATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAG 550
Qy      717 CGGAGCAGGAAAAGGACCAAGCTCAGGACCCAGGTGTGAGGCTTACAAGCAGAGAAAGGAGC 776
Db      551 CGGACAGTGAAGGAAGGACCAAGCTCAGGACCCAGGTGTGAGGCTTAMAAGCAGAGAAAGGAGC 610
Qy      777 ACTGTGTGGGCATCGTGTCTGAACTGCACTCAAGCTCAAGCTCAAGCGGCTCCTCAGAG 836
Db      611 ACTGTGTGGGCATCGTGTCTGAACTGCACTCAAGCTCAAGCTCAAGCGGCTCCTCAGAG 670
Qy      837 ATTCTCTTGTGAAATTTAGGATGGCTGAAGGAGAACGAGAGGTTCAGTAAAAAGAAATCA 896
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Qy      897 AGCATAGTCTCTGGGCCACGAGAACAGTCTCCACTCGCCAGCGGCTTGTCTAAATATAGGA 956
Db      731 AGCATAGTCTCTGGGCCACGAGAAAGTCTCCACTGCGCAC-----GA 772
Qy      957 CGAGATCTCAGATGGGGCCAAAGAAATTAATTGAAACATGAGAGTTAACTGTGAGCCAGC 1016
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Qy      1017 TCTGCTGTGCTTAAGGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACTCAAGG 1076
Db      833 YCTGCTGTGCTTAAGGGGAAGGGATCAGAAGGTGGAGAGACTTGCARKTGCCCTCAAGG 892
Qy      1077 AGGCCCAAGAAAGAGTTTCAGATTTTGAAGAAAGAAAACAAGTAATCGTTCTGAGATTGAAA 1136
Db      893 AGSCAAAGAAAGAGTTTACG---TTTGAAGAAAGAAAMARKATCSKKCKGAGATKG-AA 948
Qy      1137 CCCAGACAGCGGGAGCACAGAGAAAGAGAAATGATGAAGA 1176
Db      949 CCCARACASAGGGGRSCMARAGAAAARAAKRWGAAGARAA 988

RESULT 26
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LOCUS      919 bp mRNA linear EST 05-APR-2004
DEFINITION AL565831 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF008YE13 3-PRIME, mRNA sequence.
ACCESSION AL565831
VERSION    AL565831.3 GI:46232652
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 919)
AUTHORS    Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE      Full-length cDNA libraries and normalization
JOURNAL    Unpublished (2001)
COMMENT    On Feb 16, 2001 this sequence version replaced gi:30550229.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, Cp 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr

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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized. Library was constructed by Life Technologies, a division of Invitrogen.

This sequence belongs to sequence cluster 5584.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DF008AC07NP1&c=5584.f.

FEATURES

Location/Qualifiers

1..919

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DF008YE13"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

/clone\_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

ORIGIN

Query Match 35.9%; Score 746.2; DB 1; Length 919;  
Best Local Similarity 95.2%; Pred. No. 1e-181;  
Matches 774; Conservative 24; Mismatches 11; Indels 4; Gaps 3;

QY 1170 ATGAGAGAAAGCCCGGAGACTGTGGAAAGGAGTGAAGCACTGAACCTCCAGGTGA 1229

DB 919 ATGAAGAGAAAGCCCGGAGACTGTGGAAAGGAGTGAAGCACTGAACCTCCAGGTGA 860

QY 1230 CATCTCTGTTTAAGAGCTTCAAGAGGCTCATAC-AAAACCTCAGCGAGCTCAGCTAATG 1288

DB 859 CATCTCTGTTTAAGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAGCTCAGCTAATG 800

QY 1289 AAGAAGAGACTTCAAGAAAGTGTGAGGCCCTTGAAGGAAAAATTTGCAATTCATCA 1348

DB 799 AAGAAGAGACTTCAAGAAAGTGTGAGGCCCTTGAAGGAAAAATTTGCAATTCATCA 740

QY 1349 GAGTTGAATGAAGCAAGAGCTGTTTATCTAACAATAAGTTAGAGCTACAAGTGA 1408

DB 739 GAGTTGAATGAAGCAAGAGCTGTTTATCTAACAATAAGTTAGAGCTACAAGTGA 680

QY 1409 AGCATGCTATCAAAATCAAAATGGAACAGGCTTAAACAGAGATGAAAAGTCCAAATTA 1468

DB 679 AGCATGCTATCAAAATCAAAATGGAACAGGCTTAAACAGAGATGAAAAGTCCAAATTA 620

QY 1469 ACTGTGCTACAGATGACACAAAGCTTCTTCAAGAACATAATATGCAATTGAAAAA 1528

DB 619 ACTGTGCTACAGATGACACAAAGCTTCTTCAAGAACATAATATGCAATTGAAAAA 560

QY 1529 ATTGAGGAATCAACAGAAAAGAGTCAGAAAAGTGGACAGGCGAGTGTGAAGAACTG 1588

DB 559 ATTGAGGAATCAACAGAAAAGAGTCAGAAAAGTGGACAGGCGAGTGTGAAGAACTG 500

QY 1589 AGTGAATAAACTGGAAGCTGCGAGAGGCTCTGGCTTCCAAACAGCTGCAATGGATGA 1648

DB 499 AGTGAATAAACTGGAAGCTGCGAGAGGCTCTGGCTTCCAAACAGCTGCAATGGATGA 440

QY 1649 ATGAAGCAAAACCATTCGCCAAGCAGGAAGAGGACCTGGAAACCATGACCATCTCAGGGCT 1708

DB 439 ATGAAGCAAAACCATTCGCCAAGCAGGAAGAGGACCTGGAAACCATGACCATCTCAGGGCT 380

QY 1709 CAGATGGAAGTTTACTGTTCTGATTTTTCATGTTTGAAGAGAGGCGAGAGAAATTCAT 1768

DB 379 CAGATGGAAGTTTACTGTTCTGATTTTTCATGTTTGAAGAGAGGCGAGAGAAATTCAT 320

QY 1769 GAGGAAAAGGAGCAACTGGCATTGCACTGGCAGTGTCTGCTGAAAGAGAAATGATCTTTC 1828

DB 319 GARRAAAAGGAGCAACTGGCATTGCACTGGCAGTGTCTGCTGAAAGAGAAATGATCTTTC 260

QY 1829 GAAGACGGAGGCGAGGAGTCCTTTGATGGAGATGCGAGAGTCGTGATGGGCGAGAACAGT 1888

DB 259 GAAGACGGAARCAAGCAGWCCTTGATGRAGATGCAGAGTCVTCATGTGGCGGAGAACAGT 200

QY 1889 GACTCTGACCAAGCAGGCTTACCTTTTCAAGAGAGAGCTGAGACAGGACTGGC-GGCA 1947

DB 199 GAAWCTVACCAAGCAGWCTTACCTTGATCAAGAGAGAGCTGAGVACAGGACTGGCTSGCC 140

QY 1948 ACAGCGG--AATATTCCGATTTCATCTCTGCCCC 1978

DB 139 ACAGCGGASATAATYCCGAKTCATCTCTGCCCS 107

RESULT 27

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

1 (bases 1 to 900)

Li W.B., Gruber C., Jessee J. and Polayes D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope

On May 15, 2003 this sequence version replaced gi:30787815.

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 5584.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DE013AF10QPI&c=5584.f.

Location/Qualifiers

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/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DE013YK19"

/tissue\_type="PLACENTA"

/clone\_lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed

with a NotI-oligo(dT) primer. Five prime end enriched,

double-strand cDNA was digested with Not I and cloned into

the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized."

Query Match 35.9%; Score 744.8; DB 4; Length 900;

Best Local Similarity 99.6%; Pred. No. 2.4e-181;

Matches 757; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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DB 141 CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCTCCTCACTGAAAGGAGGACGCC 200

QY 357 CAGTGAAGACACAGGAAATGACCCCCCAGCTGGCCCCACCCAACTGGACAGCTTTA 416

DB 201 CAGTGAAGACACAGGAAATGACCCCCCAGCTGGCCCCACCCAACTGGACAGCTTTA 260

QY 417 CCCCGAGGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCAAGAACCAACAGCTGAAAG 476

DB 261 CCCCGAGGAGCTGCTGCAGCAGATGAAGAGCTCTCTGACCGAGAACCAACAGCTGAAAG 320

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Qy	537	CAGAGAAACAGAGGAGAGAGCCAGTTTTCAGATACAGAGCAAGAGCAAGAGAGC	596
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Qy	597	GTCTAATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAGAGCTTTGAAAACTAAAAG	656
Db	441	GTCTAATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAGAGCTTTGAAAACTAAAAG	500
Qy	657	GGAATCAGAAAGTCTATGAGAGCCCACTGATGATCTCCAGGCTTCCAGGGCCGGAAG	716
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Qy	717	CGAGCAGGAGAAAGGACCACTCAGGACCCAGGTGGTGAGGCTACAGCAGAGAGGCAG	776
Db	561	CGAGCAGGAGAAAGGACCACTCAGGACCCAGGTGGTGAGGCTACAGCAGAGAGGCAG	620
Qy	777	ACCTGTTGGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG	836
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Qy	837	ATTCTTTTGTGAAATTTAGATGGCTGAAGGAGAGCAGAGAGGCTCAGTAAAAAGAAATCA	896
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Qy	897	AGCATAGTCTCT-GGGCCACAGAACAGTCTCCACTGGCAGCGCATTTGTTAAATATAGG	955
Db	741	AGCATAGTCTCTGGGGCCCAAGAACAGTCTCACTGGCAGCGCATTTGTTAAATATAGG	800
Qy	956	AGCAGATCTGCAGATGGGGCCAAAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAG	1015
Db	801	AGCAGATCTGCAGATGGGGCCCAAGAAATTAATCTCGAACATGAGGAGTTAACTGTGAGCCAG	860
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LOCUS			
DEFINITION			
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IMAGE:30515251 5', mRNA sequence.			
CF456387			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
Hominidae; Homo.			
NIH-MGC http://mgi.nci.nih.gov/			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
Contact: Daniela S. Gerhard, Ph.D.			
Office of Cancer Genomics			
National Cancer Institute			
Bldg. 31 Rm10A07 Bethesda, MD 20892			
Email: cgaops-r@mail.nih.gov			
Tissue Procurement: Dr. James R. Lupski			
cDNA Library Preparation: Invitrogen Corp			
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone Distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNL at:			
http://image.lnl.gov			
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High quality sequence stop: 730.			

FEATURES		Location/Qualifiers	
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		/lab_host="DH10B (T1 phage-resistant)"	
		/clone_lib="Lupski anterior horn"	
		/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 2.1 kb. Library was constructed by Invitrogen and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine)."	
ORIGIN			
Query Match		35.1%; Score 730; DB 5; Length 761;	
Best Local Similarity		99.9%; Pred. No. 1.6e-177;	
Matches 730; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
QY	861	CTGAAGGAGAGCAGAGGGTCAAGTAAAGAAATCAAGCATAGTCTCTGGGCCCCACAGAA	920
DB	31	CTGAAGGAGAGCAGAGGGTCAAGTAAAGAAATCAAGCATAGTCTCTGGGCCCCACAGAA	90
QY	921	CAGTCTCCACTGCGACGGCAATTTCTTAAATATAGGAGCAGATCTGCAGATGGGGCCCAAGA	980
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QY	981	ATTACTTCGAAACATGAGGAGTTAACTGTGAGCCAGCTCTGTGTGCCTTAAGGGAAGGGA	1040
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QY	1041	ATCAGAGGTGAGAGACTTGAAGTTGCACCTCAAGAGGCCCAAGAAAGAGTTTCAGATT	1100
DB	211	ATCAGAGGTGAGAGACTTGAAGTTGCACCTCAAGAGGCCCAAGAAAGAGTTTCAGATT	270
QY	1101	TTGAAAAGAAAAACAAGTAACTCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACAGAGA	1160
DB	271	TTGAAAAGAAAAACAAGTAACTCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACAGAGA	330
QY	1161	AGAGAAATGATGAAGAGAAAGCCCGGAGACTGTTGGAAAGCGAAGTGGAAAGCACTGAACC	1220
DB	331	AGAGAAATGATGAAGAGAAAGCCCGGAGACTGTTGGAAAGCGAAGTGGAAAGCACTGAACC	390
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QY	1341	TTCCATCAGAGTTGAATGAAAAGCAGAGCTTGTTTATACTAACAAAAAGTTAGAGCTAC	1400
DB	511	TTCCATCAGAGTTGAATGAAAAGCAGAGCTTGTTTATACTAACAAAAAGTTAGAGCTAC	570
QY	1401	AAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAACAGGCTTAAACAGAGATGAAAAGT	1460
DB	571	AAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAAACAGGCTTAAACAGAGATGAAAAGT	630
QY	1461	CCAAATTAAGTGTGCTACAGATGACACACAAACAGCTTCTTCAAGAACATATATATGCT	1520
DB	631	CCAAATTAAGTGTGCTACAGATGACACACAAACAGCTTCTTCAAGAACATATATATGCT	690
QY	1521	TGAAAAACAATTGAGGAACCTTAAACAGAAAAAGAGTCAGAAAAAGTGGACAGGCGAGTCTGA	1580
DB	691	TGAAAAACAATTGAGGAACCTTAAACAGAAAAAGAGTCAGAAAAAGTGGACAGGCGAGTCTGA	750
QY	1581	AGGAACCTGAGT	1591
DB	751	ANGAACTGAGT	761

RESULT 29	AL538121	989 bp	mrna	linear	EST 24-MAR-2004
LOCUS	AL538121				
DEFINITION	AL538121 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone				
ACCESSION	CS0DF029YP05	5-PRIME, mRNA			
VERSION	AL538121				
KEYWORDS	AL538121.3	GI:45713865			
SOURCE	EST.				
ORGANISM	Homo sapiens (human)				
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	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;				
	Hominidae; Homo.				
REFERENCE	1 (bases 1 to 989)				
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.				
TITLE	Full-length cDNA libraries and normalization				
JOURNAL	Unpublished (2001)				
COMMENT	On Feb 13, 2001 this sequence version replaced gi:31262722.				
	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE				
	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr				
	1st strand cDNA was primed with a NotI-oligo(dr) primer. Five primer				
	into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library				
	was not normalized. Library was constructed by Life Technologies, a				
	division of Invitrogen.				
	This sequence belongs to sequence cluster 5584.f				
	For more information about this cluster, see				
	<a href="http://www.genoscope.cns.fr/cdna?ts=CS0DF029YP05&amp;seq=5584.f">http://www.genoscope.cns.fr/cdna?ts=CS0DF029YP05&amp;seq=5584.f</a> .				

FEATURES	source	Location/Qualifiers
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		/db_xref="taxon:9606"
		/clone="CS0DF029YP05"
		/tissue_type="FETAL BRAIN"
		/dev_stage="fetal"
		/clone_lib="Homo sapiens FETAL BRAIN"
		/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
ORIGIN		
	Query Match	35.1%; Score 728; DB 1; Length 989;
	Best Local Similarity	97.4%; Pred. No. 5.6e-177;
	Matches	773; Conservative 8; Mismatches 5; Gaps 4;
Qy	297	CAGGAATCTTCGCAATGCCCATCAACTCTCAGCTGCCTCAGTGAAGGAGGACAGCC 356
Db	199	CAGGAATCTTCGCAATGCCCATCAACTCTCAGCTGCCTCAGTGAAGGAGGACAGCC 258
Qy	357	CCAGTGAAGCACAGGAAATGGACCCGCCACCTGGCCCCACCCAAACCTGGACACGTTTA 416
Db	259	CCAGTGAAGCACAGGAAATGGACCCGCCACCTGGCCCCACCCAAACCTGGACACATTTA 318
Qy	417	CCCCGAGGAGCTCTCCAGCAGATGAAGAGCTCCTGACCAAGAACCCACCGCTGGAAG 476
Db	319	CCCCGAGGAGCTCTCCAGCAGATGAAGAGCTCCTGACCGAGAACCCACCGCTGGAAG 378
Qy	477	AAGCCATGAAGCTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTCGGCCTGGA 536
Db	379	AAGCCATGAAGCTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTCGGCCTGGA 438
Qy	537	CAGGAACACGAGGAGACGCCAGTTTTTTTGATACAGAGCAAGAGCAAGAGC 596
Db	439	CAGGAACACGAGGAGAGACGCCAGTTTTTTTGATACAGAGCAAGAGCAAGAGC 498
Qy	597	GTCTAATGGCCTTGAGTCATGAGAAATGAGAAATTTGAAGGAGAGCTTGGAAAACTAAAG 656

/clone\_lib="Lupski\_dorsal\_root\_ganglion"  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
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5'-TCGACCCACAGGCTCGG-3' and  
5'-GACTAGTCTAGATCGGAGCGGCCCT(15)-3'. Size selected >  
1 kb for average insert length 1.7 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

## ORIGIN

Query Match 34.9%; Score 725.6; DB 3; Length 872;  
Best Local Similarity 99.1%; Pred. No. 2.2e-176;  
Matches 739; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

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Db 111 CAGGAACCTTGCATCTCCATCAACCTCTCAGCTGCCTCCTCACTGAAAAGGAGACAGCC 170  
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QY 357 CCAGTGAAGACAGAGGAATGGACCCGCCACCTGGCCACCCAAACCTGGACACGTTTA 416  
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Db 171 CCAGTGAAGACAGAGGAATGGACCCGCCACCTGGCCACCCAAACCTGGACACGTTTA 230  
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QY 417 CCCGGAGGAGCTGCTGCAGCAGATGAAGAGCTCTTGACCAAGAACCCACAGCTGAAG 476  
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Db 231 CCCGGAGGAGCTGCTGCAGCAGATGAAGAGCTCTTGACCGAGAACCCACAGCTGAAG 290  
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QY 477 AAGCCATGAGCTTAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCTTGA 536  
|||||  
Db 291 AAGCCATGAGCTTAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCTTGA 350  
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QY 537 CAGAGAAACAGAGGAAGAGCGCAGTTTTTTCAGATACAGACCAAGAGCAAGAGAGC 596  
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QY 597 GTCTAATGGCTTTGAGTCATGAGAAATGAGAAATTTGAAGGAAGAGCTTGGAAAACTAAAAG 656  
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Db 411 GTCTAATGGCTTTGAGTCATGAGAAATGAGAAATTTGAAGGAAGAGCTTGGAAAACTAAAAG 470  
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QY 657 GGAATCAGAAAGGTCTATGAGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG 716  
|||||  
Db 471 GGAATCAGAAAGGTCTATGAGAGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG 530  
|||||

QY 717 CGCAGCAGGAAAAGGACCACTCAGGACCCAGCTGAGGCTTACAGCAGAGAGGCGAG 776  
|||||  
Db 531 CGCAGCAGGAAAAGGACCACTCAGGACCCAGCTGAGGCTTACAGCAGAGAGGCGAG 590  
|||||

QY 777 ACCTGTTGGGCATCGTGTCTGAACTGCAAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG 836  
|||||  
Db 591 ACCTGTTGGGCATCGTGTCTGAACTGCAAGCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG 650  
|||||

QY 837 ATTCTTTTGTGAAATTTAGGATCGCTGAAGGAAGCAGAGGCTCAGTAAAAAGAAATCA 896  
|||||  
Db 651 ATTCTTTTGTGAAATTTAGGATCGCTGAAGGAAGCAGAGGCTCAGTAAAAAGAAATCA 710  
|||||

QY 897 AGCATAGTCTGGGCCCCACAGAACAGTCTCCACTGCGCAGCGCATTTGTCTAAATATAGGA 956  
|||||  
Db 711 AGCATAGTCTGGGCCCCACAGAACAGTCTCCACTGCGCAGCGCATTTGTCTAAATATAGGA 770  
|||||

QY 957 GCAGATCTGCAGATGGGGCCCAAGAAATTACTTTCGAACATGAGGAGTTAACT-GTAGCCAG 1015  
|||||  
Db 771 GCAGATCTGCAGATGGGGCCCAAGAAATTACTTTCGAACATGAGGAGTTAACTGTGAGCCAG 830  
|||||

QY 1016 CTCCTGCTGTGCTTAAGGGAGGGAA 1041  
|||||  
Db 831 CTCCTGCTGTGCTTAAGGGAGGGGA 856  
|||||

RESULT 31

AL535231

LOCUS

## DEFINITION

AL535231 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone  
CS0DF008YE13 5-PRIME, mRNA sequence.

## ACCESSION

AL535231

## VERSION

AL535231.3 GI:457111109

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

## REFERENCE

1 (bases 1 to 907)

## AUTHORS

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

## TITLE

Full-length cDNA libraries and normalization

## JOURNAL

Unpublished (2001)

## COMMENT

On Feb 13, 2001 this sequence version replaced gi:30541800.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 5584.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DF008AC07QPl&c=5584.f.

## FEATURES

Location/Qualifiers

1..907

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DF008YE13"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

/clone\_lib="Homo sapiens FETAL BRAIN"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

## ORIGIN

Query Match 34.7%; Score 721.4; DB 1; Length 907;

Best Local Similarity 97.3%; Pred. No. 2.8e-175;

Matches 750; Conservative 1; Mismatches 2; Indels 18; Gaps 1;

Db	515	GGAAATCAGAAAGGTCATCTGAGGACCCCACTGATGACTTCCAGGCTTCCAGGGCCGGAAG	574
Qy	717	CGGAGCAGGAAAAAGGACCAAGCTCAGGACCCAGGTGGTGAAGCTACAAGCAGAGAAAGGCAG	776
Db	575	CGGAGCAGGAAAAAGGACCAAGCTCAGGACCCAGGTGGTGAAGCTACAAGCAGAGAAAGGCAG	634
Qy	777	ACCTGTTGGGCACTCGTGTCTGAATGTCAGCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG	836
Db	635	ACCTGTTGGGCACTCGTGTCTGAATGTCAGCTCAAGCTCAAGCTCCAGCGGCTCCTCAGAAG	694
Qy	837	ATTCCTTTTGTGAATTAGATGGCTGAAGGAGAGCAGAAAGGTCAGTAAAGAAATCA	896
Db	695	ATTCCTTTTGTGAATTAGATGGCTGAAGGAGAGCAGAAAGGTCAGTAAAGAAATCA	754
Qy	897	AGCATAGTCTGGGCCACGAGAACAGTCTCCACTGGCACGGCATTGCTCTAAATATAGGA	956
Db	755	AGCATAGTCTGGGCCACGAGAACAGTCTCCACTGGCAC-----GA	796
Qy	957	CGAGATCTCGAGATGGGGCCAGAAATTACTTCAACATGAGGAGTTAACTGTAGCCAGC	1016
Db	797	CGAGATCTCGAGATGGGGCCAGAAATTACTTCAACATGAGGAGTTAACTGTAGCCAGC	856
Qy	1017	TCCTGCTGTCTTAAGGGAAGGGAATCAGAAGTGGAGAGACTTGAAGTTG	1067
Db	857	TCCTGCTGTCTTAAGGGAAGGGAATCAGAAGTGGAGAGACTTGAAGTTG	907
RESULT 32			
DV778070			
LOCUS			
DEFINITION			
Hw Fat 56 050802 F06 Bos taurus CF-24-HW fat cDNA library Bos			
taurus cDNA, mRNA sequence.			
ACCESSION			
DV778070			
VERSION			
DV778070.1			
KEYWORDS			
GI:82630946			
SOURCE			
EST.			
ORGANISM			
Bos taurus (cattle)			
Bos taurus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;			
Pecora; Bovidae; Bovinae; Bos.			
REFERENCE			
AUTHORS			
Yoon,D.H., Lee,S.H., Park,E.W., Cho,Y.M., Lee,J.H., Kim,H.,			
Kim,H.Y., Park,J.H. and Oh,S.J.			
TITLE			
Gene Expression Profiling of the Bovine liver, adipose, and			
skeletal muscle			
JOURNAL			
COMMENT			
Unpublished (2005)			
Contact: Dr. Du-Hak Yoon			
National Livestock Research Institute, RDA			
564 Omockchun-dong, Suwon, 441-350, Korea			
Tel: 82 31 290 1593			
Fax: 82 31 290 1792			
Email: dhyoon@rda.go.kr.			
FEATURES			
source			
1..1201			
Location/Qualifiers			
/organism="Bos taurus"			
/mol_type="mRNA"			
/db_xref="taxon:9913"			
/sex="Four males mixed"			
/cell_type="adipocyte"			
/dev_stage="24 months old"			
/lab_host="XLI-BlueMRF' strain"			
/clone_lib="Bos taurus CF-24-HW fat cDNA library"			
/note="Organ: adipose tissue; Vector: Uni-ZAPXR; Site_1:			
EcoRI; Site_2: Xho I"			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
833; Conservative			
0; Mismatches			
149; Indels			
6; Gaps			
2;			
Qy	1095	CAGATTTTGAAGAAAAACAGTAATCGTTCTCAGATTGAAACCCAGACAGAGGGAGCA	1154
Db	29	CTGATTTTGAAGAAAAACAGTAATCGTTCTCAGATTGAAACCCAGACAGAGGGAGCA	88

Qy	1155	CAGAAAAAGAGATGATCAAGAGAAAGCCCGGAGACTGTTGGAAAGCGAAGTGGAAACAC	1214
Db	89	CAGAAACAGAGAAAGAGAGAGAGAAAGACACCCAAACTATTGGAAAGTGAAGTGAACAC	148
Qy	1215	TGAACCTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCG	1274
Db	149	TGAACCTTCCAGGTGACAAACCCCTGTTTAAAGGAGCTTCAAGAAAGCTCACAAGAACTCAGTG	208
Qy	1275	AAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTCAAGCCCTTGAAGAGAAAAAT	1334
Db	209	AAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTCAAGCCCTTGAAGAGAAAAAT	268
Qy	1335	CTGCAATTCATCAGAGTTGAATGAAAAGCAGAGCTTGTTTATATCTAACAAAAAGTTAG	1394
Db	269	CTGCAAGCCCATCAGAACTGAATGAAAACAAAGAGCTGGTTTATAAAAACAAAAAGTTAG	328
Qy	1395	AGTACAAGTGGAAAGCATGCTATCAGAAAATCAAAATGGAACAGGCTTAAACAGAGGATG	1454
Db	329	AGCTCCAAGTGGAAAGCATGCGATCAGAAAATCAAAATGGAACAAAGCTTAAACAGAGATG	388
Qy	1455	AAAAGTCCAAATTAATCTGTCTACAGATGACACAAACAAGCTTCTTCAAGAACATAATA	1514
Db	389	AAAAGTCCAGATTAGGCACTTACAGTTGACACAAACAGGCTTCTTCAAGAAATCAATA	448
Qy	1515	ATGCATTGAAAAACAATTGAGGAACTAAACAAGAAAAAGAGTCAGAAAAAGTGACAGGCAG	1574
Db	449	ATGCATTGAGACAAATTGAGGAACTGAAAAGGAGAGAGTCAGAAAAAGTGGATAAGTGG	508
Qy	1575	TGCTGAAGAACTGAGTGAATAAATCTGGAACCTGGGAGAGAGGCTCTGGCTTCCAAACAGC	1634
Db	509	TGCTGCAGAACTGAGTGGAAAAAGCTAGAACTGGCAGAGAAAGCCCTTGGCTTCCAGACAGC	568
Qy	1635	TGCAATGGATGAATGAAGCAAAACCATTCGCAACGACGAGAGACCTGGAAAAACCATCA	1694
Db	569	TCCAAATGGATGGGATGAAGCAGACCATTCGCAACGAGGAGAGACCTGGAGACCATGG	628
Qy	1695	CCATCCTCAGGGCTCAGATGGAAAGTTTACTGTCTGATTTTTCATGCTGAAAGAGCAGCGA	1754
Db	629	CTGTCTCTCAGGGCTCAGATGGAGGTTTATTGTTCTGATTTTTCATGCTGAAAGAGCAGCAA	688
Qy	1755	GAGAGAAATTTTCATGAGGAAAAAGGAGCAACTGGCAATTCAGCTGGCAGTTCTGCTGAAAG	1814
Db	689	GAGAGAAATTTTCATGAGGAAAAAGGAGCACTGGCAATTCAGCTGGCAGTTCTGCTGAAAG	748
Qy	1815	AGAATGATGCTTTTTCGAAGACGGAG--GCAGGACGTCTTGTGATGGAGATGCAGAGTCGTC	1871
Db	749	AAAACAATGCTTTTCCAGATGGAGGAGCAGCAGGACAGACCTTGATGGGAATGCAGAACCGTC	808
Qy	1872	ATGGGGCGAGAACAAAGTGACTCTGACCAGCGGCTTACCTTTTCAAAGAGGAGCTGAGG	1931
Db	809	ATGGGGCGAGAGCAAGTGACGCTGAACAGCAGCGCTTATCTCGTTTCAAGAGGACCAAGG	868
Qy	1932	ACAGGAGCTGGCGGCAACAG----CGGAATATTCGGAATTCATTCCTGCCCCCAAGTGGAG	1988
Db	869	ATAGAAACTGGCTGCAGCAGCAACAAAAAATTCCTCATTTCTTGTGCCCCCAATGTGGAA	928
Qy	1989	AGGTTCTGCTGACATAGACAGTTTACAGATTCAGCTGATGATTCATCATTTTAAGTGT	2048
Db	929	GAGTTCTGCTGACATAGATTTCACTACTGAAATCTTGTACGGACTGTATCTTTTAAGTGT	988
Qy	2049	TGATGTATCACCTCCCCAAAACCTGTTGG	2076
Db	989	TGACCTTTTACCTCCCCCAGCTGGTTG	1016
RESULT 33			
BQ951546			
LOCUS			
DEFINITION			
BQ951546			
AGENCOURT 8923221 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6472500			
5', mRNA sequence.			
ACCESSION			
BQ951546			
VERSION			
BQ951546.1			
GI:22367024			

Query Match 34.5%; Score 717.6; DB 10; Length 1201;  
Best Local Similarity 84.3%; Pred. No. 2.9e-174;  
Matches 833; Conservative 0; Mismatches 149; Indels 6; Gaps 2;  
Qy 1095 CAGATTTTGAAGAAAAACAGTAATCGTTCTCAGATTGAAACCCAGACAGAGGGAGCA 1154  
Db 29 CTGATTTTGAAGAAAAACAGTAATCGTTCTCAGATTGAAACCCAGACAGAGGGAGCA 88





Matches	705;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
QY	1372	TCGTTTATCTACACAAAAGCTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAAT	1431						
Db	1	TGTTTATCTACACAAAAGCTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAAT	60						
QY	1432	GGACAGGCTAAACACAGAGGATGAAAGTCCAAATTTAACTGTGCTACAGATGACACAA	1491						
Db	61	GGACAGGCTAAACACAGAGGATGAAAGTCCAAATTTAACTGTGCTACAGATGACACAA	120						
QY	1492	CAAGCTCTTCAAGAACATAATATGCAATGTAATAAATGAGGAACATAACAGAAAGA	1551						
Db	121	CAAGCTCTTCAAGAACATAATATGCAATGTAATAAATGAGGAACATAACAGAAAGA	180						
QY	1552	GTCCAGAAAAGTGGACAGGCGAGTCTGAAGCACTGAGTGAAGAACTGGAACCTGGCAGA	1611						
Db	181	GTCCAGAAAAGTGGACAGGCGAGTCTGAAGCACTGAGTGAAGAACTGGAACCTGGCAGA	240						
QY	1612	GAAGGCTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAAGCAAAACCATTTGCCAAGCA	1671						
Db	241	GAAGGCTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAAGCAAAACCATTTGCCAAGCA	300						
QY	1672	GGAAAGGACCTGGAAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGA	1731						
Db	301	GGAAAGGACCTGGAAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGA	360						
QY	1732	TTTTTCATGCTGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGGAGCAACTGGCATT	1791						
Db	361	TTTTTCATGCTGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGGAGCAACTGGCATT	420						
QY	1792	GCAGCTGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTCGAAGACGGAGGAGGAGTCCTT	1851						
Db	421	GCAGCTGGCAGTTCTGCTGAAAGAGAAATGATGCTTTTCGAAGACGGAGGAGGAGTCCTT	480						
QY	1852	GATGAGATGCAAGTCTGCTATGGGCGAGAACAGATGACTCTGACGAGGAGGCTTACCT	1911						
Db	481	GATGAGATGCAAGTCTGCTATGGGCGAGAACAGATGACTCTGACGAGGAGGCTTACCT	540						
QY	1912	TGTTCAAAGAGGAGCTGAGCAGAGGAGCTGGCGCAACAGCGGAATATTCGGATTCATTC	1971						
Db	541	TGTTCAAAGAGGAGCTGAGCAGAGGAGCTGGCGCAACAGCGGAATATTCGGATTCATTC	600						
QY	1972	CTGCCCCAAGTGTGGAGAGGTTCTGCTGACATAGACACAGTTTACAGATTACGTGATGA	2031						
Db	601	CTGCCCCAAGTGTGGAGAGGTTCTGCTGACATAGACACAGTTTACAGATTACGTGATGA	660						
QY	2032	TTGCATCATTTAAGTGTGATGATATCACCTCCCAAAAACCTGTTGGT	2077						
Db	661	TTGCATCATTTAAGTGTGATGATATCACCTCCCAAAAACCTGTTGGT	706						

RESULT 35  
BQ218575  
LOCUS  
DEFINITION BQ218575 878 bp mRNA linear EST 02-MAY-2002  
5', mRNA sequence.  
ACCESSION BQ218575  
VERSION BQ218575.1 GI:20399975  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo.  
1 (bases 1 to 878)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: ATCC/DCTD/BTP  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13294 row: e column: 14  
High quality sequence stop: 564.  
Location/Qualifiers  
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/organism="Homo sapiens"  
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/clone="IMAGE:6047221"  
/tissue\_type="melanotic melanoma"  
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/clone\_lib="NIH MGC 72"  
/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2 kb. Library constructed by Life Technologies."

ORIGIN

Query Match	33.6%;	Score 697.4;	DB 3;	Length 878;
Best Local Similarity	97.8%;	Pred. No. 4.6e-169;	Mismatches 0;	Indels 5;
Matches	749;	Conservative	12;	Gaps 4;
QY	297	CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCTCTACTGAAAAGGAGGACAGCC	356	
Db	105	CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCTCTACTGAAAAGGAGGACAGCC	164	
QY	357	CCAGTGAAGCAGAGAAATGGACCCCTGCTGGCCACCCAAACCTGTGGAACGCTTTA	416	
Db	165	CCAGTGAAGCAGAGAAATGGACCCCTGCTGGCCACCCAAACCTGTGGAACGCTTTA	224	
QY	417	CCCCGGAGAGCTGCTGAGCAGATGAAGAGCTCTGACCAAGAACCCACGAGCTGAAAG	476	
Db	225	CCCCGGAGAGCTGCTGAGCAGATGAAGAGCTCTGACCAAGAACCCACGAGCTGAAAG	284	
QY	477	AAGCCATGAAGCTAAATTAATCAAGCATGAAAGGAGATTTGAGGAGCTTTCCGGCTGGA	536	
Db	285	AAGCCATGAAGCTAAATTAATCAAGCATGAAAGGAGATTTGAGGAGCTTTCCGGCTGGA	344	
QY	537	CAGAAAACAGAAAGAAACGCCAGTTTTTTTGTAGATACAGAGCAAAAGAAAGAGC	596	
Db	345	CAGAAAACAGAAAGAAACGCCAGTTTTTTTGTAGATACAGAGCAAAAGAAAGAGAGC	404	
QY	597	GTCTAATGSCCTTGAGTCATGAGATGAGAAATTCGAAGAGAGCTTGGAAAACCTAAAAG	656	
Db	405	GTCTAATGSCCTTGAGTCATGAGATGAGAAATTCGAAGAGAGCTTGGAAAACCTAAAAG	464	
QY	657	GGAAATCAGAAAGGTCTCTGAGGACCCACCTGATGACTCCAGGCTTCCAGGCGCGAAG	716	
Db	465	GGAAATCAGAAAGGTCTCTGAGGACCCACCTGATGACTCCAGGCTTCCAGGCGCGAAG	524	
QY	717	CGGACAGGAAAGAACCCAGCTCAGGACCCAGGTGTGAGGTACAAAGCAGAGAGGCGAG	776	
Db	525	CGGACAGGAAAGAACCCAGCTCAGGACCCAGGTGTGAGGTACAAAGCAGAGAGGCGAG	584	
QY	777	ACCTGTTGGGCATCGTGTGAACTGCAAGTCAAGCTGAACTCCAGCGGCTCCTCAGAAG	836	
Db	585	ACCTGTTGGGCATCGTGTGAACTGCAAGTCAAGCTGAACTCCAGCGGCTCCTCAGAAG	644	
QY	837	ATTCTCTTTGTTGAAATTAGGATGGCTGAAGGAGAAAGCAGAGGGTCAGTAAAAGAAATCA	896	
Db	645	ATTCTCTTTGTTGAAATTAGGATGGCTGAAGGAGAAAGCAGAGGGTCAGTAAAAGAAATCA	704	
QY	897	AGCATAGTCTGGGCGCCAGGAAACAGTCTCCACTGGGACCGCATTTCTTAATATAGGA	956	
Db	705	AGCATAGTCTGGGCGCCAGGAAACAGTCTCCACTGGGACCGCATTTCTTAATATAGGA	764	
QY	957	GCAGATCTGCAGATGGGCGCAAG-AAATTACTTTGAAACATG-AGGAGTTAACTGTGAGCCA	1014	
Db	765	GCAGATCTGCAGATGGGCGCAAG-AAATTACTTTGAAACATGAAAGTTAACTGTGAGCCA	824	

Qy 1015 G-CTCTGCTCTGCTCTAA--GGGAAGGAATCAGAAGTGGAGAGA 1057

Db 825 GCCTCGTGTGGGCTTAAGGAAGGAATCCGAAAGGGGGAGA 870

RESULT 36

CN309548

LOCUS CN309548 696 bp mRNA linear EST 16-MAY-2004

DEFINITION 17000582991172 GRN\_PRENEU Homo sapiens cDNA 5', mRNA sequence.

ACCESSION CN309548

VERSION CN309548.1 GI:47325962

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

TITLE 1 (bases 1 to 696)

AUTHORS Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G. J., Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M. S., Mandalam, R., Lebkowski, J. and Stanton, L. W.

TITLE Transcription factor characterization elucidates signaling networks that control human ES cell growth and differentiation

JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)

PUBMED 15146197

COMMENT

Contact: Brandenberger R

Regenerative Medicine

Geron Corporation

230 Constitution Drive, Menlo Park, CA 94025, USA

Tel: 650 473 8658

Fax: 650 473 7760

Email: rbrandenberger@geron.com

Insert Length: 696 Std Error: 0.00.

FEATURES

source

1..696

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/tissue\_type="embryonic stem cell, retinoic acid and mitogen-treated hES cell line H7"

/clone\_lib="GRN PRENEU"

/note="Oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryoid bodies were generated in the presence of all-trans retinoic acid and mitogens."

ORIGIN

Query Match 33.4%; Score 694; DB 8; Length 696;

Best Local Similarity 100.0%; Pred. No. 3.3e-168;

Matches 694; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 903 GTCTCTGGGCCACAGAACAGTCTCCACTGCGACGCATTGTCTAAATATAGGAGCAGAT 962

Db 1 GTCTCTGGGCCACAGAACAGTCTCCACTGCGACGCATTGTCTAAATATAGGAGCAGAT 60

Qy 963 CTGCAGATGGGGCCACAGAAATTACTTCGAACATGAGGAGTTAACTGTGAGGCAGCTCCTGC 1022

Db 61 CTGCAGATGGGGCCACAGAAATTACTTCGAACATGAGGAGTTAACTGTGAGGCAGCTCCTGC 120

Qy 1023 TGTGCTTAAGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACTCAAGGAGGCCA 1082

Db 121 TGTGCTTAAGGGAAGGGAATCAGAAGGTGGAGAGACTTGAAGTTGCACTCAAGGAGGCCA 180

Qy 1083 AAGAAACAGTTTCAGATTTTTCMAAAGAAAACAGTAATCGTCTCGAGATTCMAACCCAGA 1142

Db 181 AAGAAACAGTTTCAGATTTTTCMAAAGAAAACAGTAATCGTCTCGAGATTCMAACCCAGA 240

Qy 1143 CAGAGGGGAGCAGAGAAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTTGGAAGCG 1202

Db 241 CAGAGGGGAGCAGAGAAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTTGGAAGCG 300

Qy 1203 AAGTGGAGCACTGAACCTCAAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGSCTCAT 1262

stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GAGTGGGTG. The cell line was provided by Dr James Martin from University of Iowa. TAG\_TISSUE=Human Chondrosarcoma Grade 3 cell line mix TAG\_LIB=UI-H-FL0 TAG\_SEQ=GAGTGGGTG"

## ORIGIN

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Query Match      33.4%; Score 693; DB 3; Length 733;
Best Local Similarity 100.0%; Pred. No. 6e-168;
Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1385 AAAAGTTAGAGCTCAAGTGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAA 1444
Db 733 AAAAGTTAGAGCTCAAGTGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAA 674

QY 1445 ACAGAGGATGAAGTCCAAATTAAGTGTCTACAGATGACACACAAAGCTTCTCAA 1504
Db 673 ACAGAGGATGAAGTCCAAATTAAGTGTCTACAGATGACACACAAAGCTTCTCAA 614

QY 1505 GAACATAATAATGCAATTTGAAACAAATTTGAGGAACCTAAACAGAAAAAGAGTGCAGAAAAAGTG 1564
Db 613 GAACATAATAATGCAATTTGAAACAAATTTGAGGAACCTAAACAGAAAAAGAGTGCAGAAAAAGTG 554

QY 1565 GACAGGCGAGTGTGAAGAACTGAGTGAAGAACTGGAATCTGGCAGAGAGGCTCTGGCT 1624
Db 553 GACAGGCGAGTGTGAAGAACTGAGTGAAGAACTGGAATCTGGCAGAGAGGCTCTGGCT 494

QY 1625 TCCAAACAGCTCAATGATGAATGAGCAACCTATGCAACAGCAGGAGAGGAGGACCTG 1684
Db 493 TCCAAACAGCTCAATGATGAATGAGCAACCTATGCAACAGCAGGAGAGGAGGACCTG 434

QY 1685 GAAACCATGACCATCTCAGGGCTCAGATGGAAGTTACTGTTCTGATTTTCATGCTGAA 1744
Db 433 GAAACCATGACCATCTCAGGGCTCAGATGGAAGTTACTGTTCTGATTTTCATGCTGAA 374

QY 1745 AGACAGCGAGAGAGAAATTCATGAGGAAAGAGGACAACTGGCAATGCGAGTGGCAGTT 1804
Db 373 AGACAGCGAGAGAGAAATTCATGAGGAAAGAGGACAACTGGCAATGCGAGTGGCAGTT 314

QY 1805 CTGCTGAAGAGAAATGATGCTTTGGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 1864
Db 313 CTGCTGAAGAGAAATGATGCTTTGGAAGACGAGGAGGAGGAGGAGGAGGAGGAGGAG 254

QY 1865 AGTCGTGATGGGCGAGAAACAAAGTGACTCTGACGAGAGGCTTACCTTGTTCAGAGAGGA 1924
Db 253 AGTCGTGATGGGCGAGAAACAAAGTGACTCTGACGAGAGGCTTACCTTGTTCAGAGAGGA 194

QY 1925 GCTGAGGACAGGAGCTGCGGGCAACAGCGGAATATTCGGAATTCATTCCTGCCCCAAGTGT 1984
Db 193 GCTGAGGACAGGAGCTGCGGGCAACAGCGGAATATTCGGAATTCATTCCTGCCCCAAGTGT 134

QY 1985 GGAGAGGTTCTGCTGACATAGACAGGTTACAGATTCACGTGATGATGATGATGATGATGAT 2044
Db 133 GGAGAGGTTCTGCTGACATAGACAGGTTACAGATTCACGTGATGATGATGATGATGATGAT 74

QY 2045 GTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2077
Db 73 GTGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 41
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## RESULT 38

BQ879423  
LOCUS BQ879423  
DEFINITION AGENCOURT 8119646 Lupski dorsal root ganglion Homo sapiens cDNA  
clone IMAGE:6177842 5', mRNA sequence.  
ACCESSION BQ879423  
VERSION BQ879423.1 GI:22271431  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.  
REFERENCE 1 (bases 1 to 904)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Agencourt Bioscience Corporation  
Cloned through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM13556 row: h column: 03  
High quality sequence stop: 636.

FEATURES  
source

1..904  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6177842"  
/sex="male"  
/tissue\_type="dorsal root ganglia"  
/dev\_stage="adult, 36 yr"  
/lab\_host="DH10B"  
/clone\_lib="Lupski dorsal root ganglion"  
/note="Vector: pCMV-SPORT6 (Life Technologies); Site\_1:  
NotI; Site\_2: SalI; cDNA made by oligo-dT priming.  
Directionally cloned using the following adaptors:  
5'-TCGACCTTCAGTTCGCGCGCG-3' and  
5'-GACTAGTTCTAGATCGCGCGCGCCT(15)-3'. Size selected >  
1 kb for average insert length 1.7 kb. This is a primary  
library, non-amplified. Library constructed by Life  
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor  
College of Medicine) and is available through Life  
Technologies."

## ORIGIN

```
Query Match      33.3%; Score 690.8; DB 3; Length 904;
Best Local Similarity 99.3%; Pred. No. 2.4e-167;
Matches 714; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

QY 297 CAGGAACCTTCTGCAATGTCCCATCAACTCTCAGCTGCTCACTGAAAGAGGAGCAGCC 356
Db 184 CAGGAACCTTCTGCAATGTCCCATCAACTCTCAGCTGCTCACTGAAAGAGGAGCAGCC 243

QY 357 CCAGTGAAGCACAGGAATGGACCCCGCCACCTGGCCACCCAACTGGACACGTTTA 416
Db 244 CCAGTGAAGCACAGGAATGGACCCCGCCACCTGGCCACCCAACTGGACACGTTTA 303

QY 417 CCCCAGGAGCTGCTGCAGCAGATGAAAGAGCTCCTGACCAAGAACCAACAGCTGAAAG 476
Db 304 CCCCAGGAGCTGCTGCAGCAGATGAAAGAGCTCCTGACCGAGAACCAACAGCTGAAAG 363

QY 477 AAGCCATGAAGCTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTCCGCTGGA 536
Db 364 AAGCCATGAAGCTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTCCGCTGGA 423

QY 537 CAGGAAACAGAGGAAGAACGCCAGTTTCTTGATATCAGAGCAAGAAAGAAAAGAGC 596
Db 424 CAGGAAACAGAGGAAGAACGCCAGTTTCTTGATATCAGAGCAAGAAAGAAAAGAGC 483

QY 597 GTCTAATGGCTTGTGAGTCATGAGATGAGAAATTTGAAGGAAGAGCTTGGAAAACATAAAG 656
Db 484 GTCTAATGGCTTGTGAGTCATGAGATGAGAAATTTGAAGGAAGAGCTTGGAAAACATAAAG 543

QY 657 GGAAATCAGAAAGGTTCATCTGAGGAGCCCACTGATGACTCCAGGCTTCCAGGGCGGAG 716
```

Db 544 GGAATCAGAAAGGTCTCTGAGACCCCACTGATGACTCAGGCTTCCAGGGCCGAAG 603

Qy 717 CGGAGCAGGAAAGCAGCAGCTCAGACCCAGGTTGGTGAGCTACAAGCAGAGAGGCAG 776

Db 604 CGGAGCAGGAAAGCAGCAGCTCAGACCCAGGTTGGTGAGCTACAAGCAGAGAGGCAG 663

Qy 777 ACCTGTTGGGCATCGTCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 836

Db 664 ACCTGTTGGGCATCGTCTGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 723

Qy 837 ATTCTTTTGTGAAATTAGGATGGCTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGATCA 896

Db 724 ATTCTTTTGTGAAATTAGGATGGCTGAAGGAGAGAGAGAGAGAGAGAGAGAGAGATCA 783

Qy 897 AGCATAGTCTCGGGCCACAGAGAACAGTCTCCACTGGCAGCGCATTTCTTAAATATAGGA 956

Db 784 AGCATAGTCTCGGGCCACAGAGAACAGTCTCCACTGGCAGCGCATTTCTTAAATATAGGA 843

Qy 957 GCAGATCTGCAGATGGGG-CCAGAAATTACTTCCAACTGAGGAGTAACTGTGAGCC 1013

Db 844 GCAGATCTGCAGATGGGGCCCAAGATTACTTCCAACTGAGGAGTAACTGTGAGCC 902

## RESULT 39

AL567151/c  
LOCUS AL567151 Homo sapiens FETAL BRAIN Homo sapiens linear EST 05-APR-2004  
DEFINITION CS0DF029YP05 3-PRIME, mRNA sequence.

## ACCESSION

AL567151

## VERSION

AL567151.3 GI:46233740

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo;

1 (bases 1 to 985)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On Feb 16, 2001 this sequence version replaced gi:31290071.

Contact: Genoscope

Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with Not I and cloned

into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library

was not normalized. Library was constructed by Life Technologies, a

division of Invitrogen.

This sequence belongs to sequence cluster 5584.f

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CS0DF029CH03NP1&c=5584.f.

Location/Qualifiers

1. .985

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DF029YP05"

/tissue\_type="FETAL BRAIN"

/dev\_stage="fetal"

/notes="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

## ORIGIN

Query Match 33.0%; Score 686; DB 1; Length 985;  
Best Local Similarity 83.9%; Pred. No. 4.3e-166;  
Matches 826; Conservative 37; Mismatches 101; Indels 21; Gaps 10;

Qy 1105 AAAGAAACAAAGTAATCTGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACAGAGAAAGA 1164

Db 982 RAAAAAAGAAAGTAATCGGTGKR-KATTRAAMCCMRACAGTGGGAGCAMRRRAAGAGA 924

Qy 1165 GAATGATGAGAGAAAGGCCGAGAGACTGTTGGAGCGAAGTGGAGCAGCTGAACCTCCA 1224

Db 923 KTAIRAAGA---GAARGRCCCGAGACTGTTGAAAGCRAAGTGRAAGCAATRA--CTTCC 870

Qy 1225 GGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACTCAGCGAAAGCTGAGCT 1284

Db 869 AGTGCCATCTCTGTTTAAAGGASCTTCAAGAGGSTMATACAAACT-MGCGAAGCTGAGCT 811

Qy 1285 AATGAAGAGAGACTCTCAAGAAAAGTGTCAAGGCCCTTGAAGGAAAATTTCTGCAATTC 1344

Db 810 AATGAAGAGAGACTTTCAGAAAAGTGTCAAGGCCCTTGAAGGAAAATTTCTGMAATTC 751

Qy 1345 ATCAGAGTTTCAATGAAAAGCAAGAGCTTGTGTTTATCTAACAAGAAAGTT--AGAGCTACA 1401

Db 750 ATWAGAGTTGAAATGAAAAGCAAGAGCTTGTGTTTATCTAACAAGAAAGTTAAGAGCTACAAA 691

Qy 1402 AGTGGAAAGCATGCTATCAGAAAATCAAAA---TGGAAACAGGCTTAAACAGAGGATGAAA 1457

Db 690 NTGAAAAGCATGCTATCAGAAAATCAAAA---TGGAAACAGGCTTAAACAGAGGATGAAA 631

Qy 1458 AGTCC--AAATTAATGTGCTACAGATGA-CACACAACAAAGCTTCTTCAAGAAACA--TAA 1512

Db 630 AGTCCCAATTAATGCTGCTACAGATGACCAACAAAGAAAGTCTTMAAGAAAAATAA 571

Qy 1513 TAATGCTATGAAAACAAATTTGAGAACTTACAAAGAAAGAGTTCAGAAAAGTGGACAGGC 1572

Db 570 AATAAAATGAAAACAAATTTGAGAACTTACAAAGAAAGAGTTCAGAAAAGTGGACAGGC 512

Qy 1573 AGTGCTGAAGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGAGGCTCTGCTTCCAAACA 1632

Db 511 AGTGCTGAAGAACTGANTGAAAACCTGGAACCTGGCAGAGAGAGGCTCTGCTTCCAAACA 452

Qy 1633 GTTGCAAAATGAGTGAATGAAGCAAAACCTATGCAAGAGAGAGAGACCTGGAACCAT 1692

Db 451 NCTGCAAAATGAGTGAATGAAGCAAAACCTATGCAAGAGAGAGAGACCTGGAACCAT 392

Qy 1693 GACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGAGCAGC 1752

Db 391 GACCATCTCAGGGCTCAGATGGAAGTTTACTGTTTCTGATTTTTCATGCTGAAAGAGCAGC 332

Qy 1753 GAGAGAGAAATTCATGAGGAAAGAGCAACTGGCAATTCAGCTGGCAGTCTGCTGAA 1812

Db 331 GAGAGAGAAATTCATGAGGAAAGAGCAACTGGCAATTCAGCTGGCAGTCTGCTGAA 272

Qy 1813 AGAAGATGATGCTTTTCAAGACGGAGCAGGAGTCTTGTGATGAGATGAGAGTCTGCTCA 1872

Db 271 AGAAGATGATGCTTTTCAAGACGGAGCAGGAGTCTTGTGATGAGATGAGAGTCTGCTCA 212

Qy 1873 TGGGGCGAGAACAGTGAAGTCTGACAGAGGCTTACCTGTTTCAAGAGAGAGAGTGAAG 1932

Db 211 TGGNNCGAGAACAAATGACTCTGACAGCAGGCTTACCTTGTTCAGAGAGAGAGTGAAG 152

Qy 1933 CAGGGAGTGGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCCAAGTGTGAGAGGT 1992

Db 151 CAGGAACCTGCGMGAAACAGCGGAATATTCGATTCATTCCTGCCCCCAAGTGTGAGAGGT 92

Qy 1993 TCTGCTGACATAGACACGTTTACAGATTACAGTGGATTTGATGATGATGATGATGATGAT 2052

Db 91 TCTGCTGACATAGACACGTTTACAGATTACAGTGGATTTGATGATGATGATGATGATGAT 32

Qy 2053 GTATCATCTTCCCAAAACTGTTGGT 2077

Db 31 NTNTCNCTCCCBNAACCTGTTGGT 7

## RESULT 40

BQ773529/c

LOCUS

DEFINITION

BQ773529 723 bp mRNA linear EST 26-JUL-2002  
UI-H-FEO-bby-d-03-0-UI.s1 NCI\_GCAP\_FEO Homo sapiens cDNA clone

```

UI-H-FEO-bby-d-03-0-UI 3', mRNA sequence.
ACCESSION BQ773529
VERSION BQ773529.1 GI:21982005
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
TITLE Homnidae; Homo.
JOURNAL 1 (bases 1 to 723)
COMMENT NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
Location/Qualifiers
1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FEO-bby-d-03-0-UI"
/tissue_type="Chondrosarcoma Cell line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_FEO"
/note="Vector: pT73-Pac (Pharmacia) with a modified
polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP FEO is
a cDNA library containing the following tissue(s): a pool
of 3 chondrosarcoma cell lines (grade 2) The library was
constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
CGCTACGGAC. The cell lines was provided by Dr James Martin
of University of Iowa.
TAG_TISSUE=human grade 2 chondrosarcoma cell line pool
TAG_LIB=UI-H-FEO
TAG_SEQ=CGTACGGAC"
ORIGIN
Query Match 32.8%; Score 682; DB 3; Length 723;
Best Local Similarity 99.9%; Pred. No. 4.3e-165;
Matches 682; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1395 AGCTCAAGTGGAAAGCATGCTTATCAGAAATCAAAATGGAACAGGCTAAACAGAGGATG 1454
DB 723 AGCTCAAGTGGAAAGCATGCTTATCAGAAATCAAAATGGAACAGGCTAAACAGAGGATG 664
QY 1455 AAAAGTCCAAATTAAGTGTCTACAGATGACACACACAGCTTCTCAAGACATATA 1514
DB 663 AAAAGTCCAAATTAAGTGTCTACAGATGACACACACAGCTTCTCAAGACATATA 604
QY 1515 ATGCTATTGAAAACAAATTGAGGAACATAACAGAAAGAGTCAGAAAAGTGGACAGGCAG 1574
DB 603 ATGCTATTGAAAACAAATTGAGGAACATAACAGAAAGAGTCAGAAAAGTGGACAGGCAG 544
QY 1575 TGCTGAAGGAATGAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACAGC 1634
DB 543 TGCTGAAGGAATGAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACAGC 484

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QY 1635 TGCAAAATGGATGAATGAAGCAAAACCAATTGCCAAGCAGAAAGAGACCTGGAAAACCATGA 1694
DB 483 TGCAAAATGGATGAATGAAGCAAAACCAATTGCCAAGCAGAAAGAGACCTGGAAAACCATGA 424
QY 1695 CCATCCTCAGGGCTCAGATGGAAGTTTACTGTTCTGTATTTTCATCTGAAAGAGCAGCA 1754
DB 423 CCATCCTCAGGGCTCAGATGGAAGTTTACTGTTCTGTATTTTCATCTGAAAGAGCAGCA 364
QY 1755 GAGGAAAATTCATGAGGAAAAGGAGCAACTGGCAATTCAGCTGCGACCTCTGCTGAAG 1814
DB 363 GAGGAAAATTCATGAGGAAAAGGAGCAACTGGCAATTCAGCTGCGACCTCTGCTGAAG 304
QY 1815 AGAATGATGCTTTTGAAGACGAGGAGCGAGTCCCTGATGAGATGAGAGTCTGTCATG 1874
DB 303 AGAATGATGCTTTTGAAGACGAGGAGCGAGTCCCTGATGAGATGAGAGTCTGTCATG 244
QY 1875 GGGCGAGAACCAAGTGACTCTCACCAGCAGGCTTACCTTGTTCAAAGAGAGCTGAGGACA 1934
DB 243 GGGCGAGAACCAAGTGACTCTCACCAGCAGGCTTACCTTGTTCAAAGAGAGCTGAGGACA 184
QY 1935 GGGACTGCGGCAACAGCAGGGAATATTCGATTCATCTCTGCCCAAGTGTGGAGAGTTTC 1994
DB 183 GGGACTGCGGCAACAGCAGGGAATATTCGATTCATCTCTGCCCAAGTGTGGAGAGTTTC 124
QY 1995 TGCTTGACATAGACACAGTTACAGATTACAGTTCAGTTCATCTTAAAGTGTGATGT 2054
DB 123 TGCTTGACATAGACACAGTTACAGATTACAGTTCAGTTCAGTTCATCTTAAAGTGTGATGT 64
QY 2055 ATCACCTCCCCCAAACTGTGGT 2077
DB 63 ATCACCTCCCCCAAACTGTGGT 41

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```

RESULT 41
BQ776232/c
LOCUS BQ776232
DEFINITION UI-H-FHO-bcn-i-23-0-UI-s1 NCI CGAP FHO Homo sapiens cDNA clone
UI-H-FHO-bcn-i-23-0-UI 3', mRNA sequence.
ACCESSION BQ776232
VERSION BQ776232.1 GI:21984708
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE 1 (bases 1 to 726)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Martin
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes.
FEATURES
Location/Qualifiers
1..726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-FHO-bcn-i-23-0-UI"
/tissue_type="Human Chondrosarcoma Cell Line"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI-CGAP_FHO"
/note="Organ: Bone; Vector: pT73-Pac (Pharmacia) with a

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QY 1557 AAAAAAGTGACAGGCGAGTGTGAAGAACTGAGTGAATAAACTGGAACCTGGCAGAGAAGG 1616
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Db 562 AAAAAAGTGACAGGCGAGTGTGAAGAACTGAGTGAATAAACTGGAACCTGGCAGAGAAGG 503
|
|
|
QY 1617 CTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATGCGCAAGCAGGAAG 1676
|
|
|
Db 502 CTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATGCGCAAGCAGGAAG 443
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|
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QY 1677 AGGACCTGGAACCAATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC 1736
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|
|
Db 442 AGGACCTGGAACCAATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC 383
|
|
|
QY 1737 ATGCTGAAAGACGACGAGAGAGAAATTCATGAGAAAGAGCAACTGGCATTGCGAGC 1796
|
|
|
Db 382 ATGCTGAAAGACGACGAGAGAGAAATTCATGAGAAAGAGCAACTGGCATTGCGAGC 323
|
|
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QY 1797 TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTCGAAGACGGAGCGAGCGAGTCTTTGATGG 1856
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|
Db 322 TGGCAGTTCTGCTGAAAGAGAAATGATGCTTTCGAAGACGGAGCGAGCGAGTCTTTGATGG 263
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QY 1857 AGATGACAGTGTCTATGTTGGGGGAGAACTGAGTGAATCTGACAGCAGGCTTACCTTGTTC 1916
|
|
|
Db 262 AGATGACAGTGTCTATGTTGGGGGAGAACTGAGTGAATCTGACAGCAGGCTTACCTTGTTC 203
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|
|
QY 1917 AAGAGGAGCTGAGGACGAGGACTGCGGCAACAGCGGAATATTCGATTCAATCTCTGCC 1976
|
|
|
Db 202 AAGAGGAGCTGAGGACGAGGACTGCGGCAACAGCGGAATATTCGATTCAATCTCTGCC 143
|
|
|
QY 1977 CC-AAAGTGTGAGAGGTTCTGCTGACATAGACAGTGTACAGATTCACTGATGGATTGC 2035
|
|
|
Db 142 CCAAGTGTGAGAGGTTCTGCTGACATAGACAGTGTACAGATTCACTGATGGATTGC 83
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QY 2036 ATCATTAAAGTGTGATGATATCACCTCCCAAAA 2069
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Db 82 ATCATTAAAGTGTGATGATATCACCTCCCAAAA 49
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RESULT 43
CD245471
LOCUS
DEFINITION
AGENCOURT_14098672 NIH_MGC_181 Homo sapiens cDNA clone
IMAGE:30376546 5', mRNA sequence.
CD245471
CD245471.1 GI:31005935
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 871)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM439 row: f column: 11
High quality sequence stop: 670.
Location/Qualifiers
1..871
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30376546"
/tissue_type="White Matter"
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/dev stage="Unknown"
/lab host="DH10B-Ton A ( T1 and T5 phage resistances)"
/clone lib="NIH_MGC_181"
/notes="Vector: pCMV-SPORT6.1; Site 1: NotI; Site 2: EcoRV
(deprecated); Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.42 kb. Library was constructed by
(Invitrogen). Note: this is a NIH_MGC Library."
```

ORIGIN

Query Match	32.7%	Score 679.8	DB 5	Length 871
Best Local Similarity	99.4%	Pred. No. 1.7e-164		
Matches 693	Conservative 0	Mismatches 2	Indels 2	Gaps 1
QY	297	CAGGAACCTTCGCAATGTCCTCAACCTCTCAGCTGCCTCACTGAAAGAGGAGCAGCC	356	
Db	124	CAGGAACCTTCGCAATGTCCTCAACCTCTCAGCTGCCTCACTGAAAGAGGAGCAGCC	183	
QY	357	CCAGTGAAGACACAGGAAATGGACCCCTCCACCTGCGCCACCCAAACCTGGACACGTTTA	416	
Db	184	CCAGTGAAGACACAGGAAATGGACCCCTCCACCTGCGCCACCCAAACCTGGACACGTTTA	243	
QY	417	CCCGGAGGAGCTGCTGACGAGATGAAAGAGCTCTCTGACCAAGAACCAACAGCTGAAAG	476	
Db	244	CCCGGAGGAGCTGCTGACGAGATGAAAGAGCTCTCTGACCAAGAACCAACAGCTGAAAG	303	
QY	477	AAGCCATCAAGCTAAATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTTTCGGCTTGA	536	
Db	304	AAGCCATCAAGCTAAATAATCAAGCCATGAAGGGAGATTTGAGGAGCTTTTCGGCTTGA	363	
QY	537	CAGAAAAACAGAAAGAAAGCCAGCTTTTGTGATACAGAGCAAAAGCAAAAGAGC	596	
Db	364	CAGAAAAACAGAAAGAAAGCCAGCTTTTGTGATACAGAGCAAAAGCAAAAGAGC	423	
QY	597	GTCTAATGGCTTGTGATCATGAGATGAGAAATTTGAAGGAGAGCTTTGAAAAAAG	656	
Db	424	GTCTAATGGCTTGTGATCATGAGATGAGAAATTTGAAGGAGAGCTTTGAAAAAAG	483	
QY	657	GGAAATCAGAAAGGTCATCTGAGGACCCACTGATGATCTCCAGGCTTCCAGGGCGGAAG	716	
Db	484	GGAAATCAGAAAGGTCATCTGAGGACCCACTGATGATCTCCAGGCTTCCAGGGCGGAAG	543	
QY	717	CGGAGCAGAAAAAGGACCAAGCTCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAGGCGAG	776	
Db	544	CGGAGCAGAAAAAGGACCAAGCTCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAGGCGAG	603	
QY	777	ACCTGTTGGGCATCGTGTCTGAACTGACAGCTCAAGCTCAAGCTCCAGCGGCTCTCAGAG	836	
Db	604	ACCTGTTGGGCATCGTGTCTGAACTGACAGCTCAAGCTCAAGCTCCAGCGGCTCTCAGAG	663	
QY	837	ATTCCTTTGTTGAATAGGATGGCTGAAGGAGAGCAGAGGGTCAAGTAAAGAAATCA	896	
Db	664	ATTCCTTTGTTGAATAGGATGGCTGAAGGAGAGCAGAGGGTCAAGTAAAGAAATCA	723	
QY	897	AGCATAGTCTCGGGCCACAGAGAAAGCTCTCCACTGGCAGCGCATTTCTAAATATAGA	956	
Db	724	AGCATAGTCTCGGGCCACAGAGAAAGCTCTCCACTGGCAGCGCATTTCTAAATATAGA	783	
QY	957	GCAGATCTGCAGATGGGG--CCAAGAAATCTTCCGAA	991	
Db	784	GCAGATCTGCAGATGGGGCCCGCCAGGAATTAATCTTCGAA	820	

RESULT 44

LOCUS	602300889F1 NIH_MGC_87	Homo sapiens	cDNA clone	linear	EST 24-JAN-2001
DEFINITION	mRNA sequence.				
ACCESSION	BG031732				
VERSION	BG031732.1				
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 740)  
NIH-MGC <http://mgs.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: DCTD/DTF  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: L1AM10110 row: b column: 23  
High quality sequence stop: 675.

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Location/Qualifiers  
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/clone="IMAGE:4402102"  
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/clone\_lib="NIH\_MGC\_87"  
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#### ORIGIN

Query Match 32.3%; Score 670.8; DB 2; Length 740;  
Best Local Similarity 99.6%; Pred. No. 3.4e-162;  
Matches 683; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 1097 GATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACA 1156
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Db 10 GGTTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACA 69
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|
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QY 1157 GAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTTGGAAAGCGAAGTGGAGCACTG 1216
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|
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Db 70 GAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTTGGAAAGCGAAGTGGAGCACTG 129
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QY 1217 AACTCCAGTGACATCTCTGTTTAAGGACCTTCAAGAGGCTCATCAAAACTCAGCGAA 1276
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|
|
Db 130 AACTCCAGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATCAAAACTCAGCGAA 189
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|
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QY 1277 GCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTCCAGGCCCTTGAAGGAAAATTTCT 1336
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|
Db 190 GCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTCCAGGCCCTTGAAGGAAAATTTCT 249
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QY 1337 GCAATTCATCAGAGTTGAATGAAACCAAGAGCTGTTTATATCTAACAAAAAGTTAGAG 1396
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Db 250 GCAATTCATCAGAGTTGAATGAAACCAAGAGCTGTTTATATCTAACAAAAAGTTAGAG 309
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QY 1397 CTCAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAA 1456
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Db 310 CTCAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAA 369
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QY 1457 AAGTCCAAATTAAGTGTCTACAGATGACACAAACAGAGCTTCTCAAGAACATAATAAT 1516
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Db 370 AAGTCCAAATTAAGTGTCTACAGATGACACAAACAGAGCTTCTCAAGAACATAATAAT 429
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QY 1517 GCATTGAAAACAATTCAGGAACTAAACAAGAAAAGAGTCAGAAAAAGTGGACAGGGCAGTG 1576
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Db 490 CTGAAGGAACAGTAGTGAAAAAATTGGAACTGGGAGAGAGGCTCTGGCTTCCAAACAGCTG 549
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QY 1637 CAAATGATGAAATGAAGCAAAACCATTTGCCAAGCAGGAAGAGGACCTGGAAACCATGACC 1696
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QY 1697 ATCCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGAGCAGCAGAG 1756
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Db 610 ATCCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTTCATGCTGAAAGAGCAG-GAGA 668
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QY 1757 GAGAAAATTCATGAGGAAGAGGACCA 1782
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#### RESULT 45

AU122473  
LOCUS AU122473  
DEFINITION AU122473 MAMMAL Homo sapiens cDNA clone MAMMAL1002441 5', mRNA sequence.

ACCESSION AU122473

VERSION AU122473.1 GI:10937743

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 895)

AUTHORS Kimura, K., Wakamatsu, A., Suzuki, Y., Ota, T., Nishikawa, T., Yamashita, R., Yamamoto, J., Sekine, M., Tsuritani, K., Wakaguri, H., Ishii, S., Sugiyama, T., Saito, K., Isono, Y., Irie, R., Kushida, N., Yoneyama, T., Otsuka, R., Kanda, K., Yokoi, T., Kondo, H., Wagatsuma, M., Murakawa, K., Ishida, S., Ishibashi, T., Takahashi-Fujii, A., Sugano, S., Tanase, T., Nagai, K., Kikuchi, H., Nakai, K., Isogai, T. and Sugano, S.  
Diversification of Transcriptional Modulation: Large-scale Identification and Characterization of Putative Alternative Promoters of Human Genes  
Genome Res. 16 (1), 55-65 (2006)  
16344560

JOURNAL PUBMED

COMMENT Contact: Takao Isogai

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Helix Research Institute

2-6-7 Kazusa-Kamatari, Kisarazu, Chiba, 292-0818, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: [flj-cdna@nifty.com](mailto:flj-cdna@nifty.com)

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix

Research Institute; cDNA library construction: Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

#### FEATURES

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Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="MAMMAL1002441"  
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/clone\_lib="MAMMAL"  
/note="Vector: pME18SFL3"

#### ORIGIN

Query Match 32.0%; Score 664.2; DB 1; Length 895;  
Best Local Similarity 98.9%; Pred. No. 1.9e-160;  
Matches 699; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

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QY 297 CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAAGGAGCAGCC 356
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Db 131 CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAAGGAGCAGCC 190
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QY 357 CCAGTGAAGACACAGGAATGGACCCGCCACCTGGCCCCCAACCCAAACCTTGGACACGTTTA 416
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Db 191 CCAGTGAAGACACAGGAATGGACCCGCCACCTGGCCCCCAACCCAAACCTTGGACACGTTTA 250
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QY	417	CCCCGAGGAGCTGCTGCAGCAGATGAAGAGCTCTGACCAAGAACACACAGCTGAAAG	476
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Db	311		
QY	537	CAGAGAAACAGAGGAGAACCCAGTCTTTTTCAGATACAGACGACAAAGCAAAAGAGC	596
Db	371		
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Db	431		
QY	657	GGAATACAGAAAGGTCATCTGAGGACCCCACTGATGATCTCCAGGCTTCCAGGGCCGAG	716
Db	491		
QY	717	CGAGCAGAGAAAGGACAGCTCAGACCCAGTGGTGAGGCTACAGCAGAGAGCGAG	776
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QY	837	ATTCCTTTGTTGAAATAGATGGCTGAAGAGAGAGAGAGAGGGTCAGTAAAGAAATCA	896
Db	671		
QY	897	AGCATAGTCTGGGCCACGAGACAGCTCCACTGGCAGCGCATTTCTTAATATAGGA	956
Db	731		
QY	957	GCAGATCTCGAGATGGGGCCAGAGATTTACTTCGAAACATGAGGAGTTA 1003	
Db	790		
Db	790	-NNGATCTGCAGATGGGGCCAGAGATTACTTTG-ACATGAGGAGTTA 834	
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LOCUS	IL3-UT0117-130301-499-E06	UT0117	Homo sapiens cDNA, mRNA sequence.
DEFINITION			
ACCESSION	BI062019		
VERSION	BI062019.1	GI:14469546	
KEYWORDS	EST.		
SOURCE	Homo sapiens		
ORGANISM	Homo sapiens (human)		
REFERENCE			
AUTHORS			
1 (bases 1 to 664)			
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,			
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,			
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,			
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,			
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,D.F., de Souza,S.J. and			
Simpson,A.J.			
Shotgun sequencing of the human transcriptome with ORF expressed			
sequence tags			
Proc. Natl. Acad. Sci. U.S.A.	97 (7),	3491-3496	(2000)
10737800			
Contact: Simpson A.J.G.			
Laboratory of Cancer Genetics			
Ludwig Institute for Cancer Research			
Rua Prof. Antonio Prudente 109, 4 andar,	01509-010,	Sao Paulo-SP,	
Brazil			
Tel: +55-11-2704922			
Fax: +55-11-2707001			
Email: asimpson@ludwig.org.br			
This sequence was derived from the FAPESP/LICR Human Cancer Genome			

project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=IL3&t2=IL3-UT0117-130301-499-E06&t3=2001-03-13&t4=1)  
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High quality sequence stop: 663.  
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/dev\_stage="Adult"  
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/note="Organ: uterus tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the puc 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match	31.8%;	Score 659.8;	DB 2;	Length 664;
Best Local Similarity	99.5%;	Pred. No. 2.4e-159;		
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			Gaps	0;
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QY	1265	AAACTCAGCGAAGCTGAGCTAATGAAGAAGAGACTTCAAGAAAAAGTGTGAGGCCCTTGA	1324	
Db	604			
QY	1325	AGGAAAAATTCGCAATTCATCAGAGTTGAATGAAGAAGAGAGCTGTTTATATACTAAC	1384	
Db	544			
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QY	1565	GACAGGGCAGTGTCTGAAGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCT	1624	
Db	304			
QY	1625	TCCAAACAGCTGCAAAATGGATGAATGAAGCAAAACATTTGCCAAGCAGGAAGAGACCTTG	1684	
Db	244			
QY	1685	GAACCATGACCATCCTCAGGGCTCAGATGGAAGTTTACTGTCTGATTTTCATGCTGAA	1744	
Db	184			
QY	1745	AGAGCAGCGAGAGAGAAAAATTCATGAGGAAAGAGGACAACTGGCAATTCGAGCTGGCAGTT	1804	
Db	124			
QY	1805	CTGCTGAAAGAGATGATGCTTTCGAACGAGGAGCAGCTCCTTGTATGATGAGATGCAG	1864	
Db	64			
QY	1865	AGTC 1868		
Db	4	AGTC 1		

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RESULT 47
LOCUS      DN110950
DEFINITION 111027 MARC 4PIG Sus scrofa cDNA 5', mRNA linear EST 14-FEB-2005
ACCESSION  DN110950
VERSION     DN110950.1 GI:59789535
KEYWORDS   Sus scrofa (pig)
SOURCE     Sus scrofa
ORGANISM   Sus scrofa

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
Sus.

REFERENCE
AUTHORS    Smith,T.P.L., Freking,B.A., Ford,J.J., Vallet,J.L., Wise,T.A.,
            Nonneman,D.J., Wray,J.E. and Keele,J.W.
TITLE      Porcine EST collection using a normalized library constructed from
            embryos representing early developmental stages
JOURNAL    Unpublished (2003)
COMMENT    Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called with phred v0.020425.c and
            trimmed with the aid of the trim_alt option. Vector identified with
            cross_match v0.990329.
            Plate: HHY8005 row: H column: 8
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                        day-15, day-25, and day-30 whole embryos."

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Best Local Similarity 84.0%; Pred. No. 2.6e-159;
Matches 764; Conservative 0; Mismatches 127; Indels 18; Gaps 1;

QY      867  GAGAAGCAGAGGGTCAGTAAAGAAATCAAGCAATAGCATAGTCTGGGCCACAGAGAACAGTCT 926
DB      1   GAGAAGCAGATGAGCAATGAGGAAATCAAGCAAGTCTCTGGGCCCATTAAGAACTGATT 60

QY      927  CCACTGCACGGCATTTGCTCTAATATAGGAGCAGATCTGCAGATGGGCCCAAGATTACT 986
DB      61  CCATTGACAC-----GAGCAATCTGCAGAAAGTACCAGGAATATT 102

QY      987  TCGAATCATGAGGAGTTAACTGTGAGCAGCTCTCTGTGCTTAAGGAAAGGAAATCAGA 1046
DB      103  TGGAAATTTGAGGAATTAATCTGTGAGCCAGCTCTCTGTGCTTAAGGAAAGGAAATCAGA 162

QY      1047 AGGTGAGAGACATTGAGTTGCACTCAAGAGAGCCCAAGAAAGAGTTTCAGATTTTGA 1106
DB      163  AGGTGAGAGACATTGAAATCGCCCTCAAGGAAGCCCAAGAAAGAAATTTAGATTTTGA 222

QY      1107 AGAAACAAGTATCTGTTGAGATTGAAACCCAGACAGAGGGGAGCAGAGAAAGAGA 1166
DB      223  AGAAACCAAGGATCTGTTGAGACTGAGACCCAGACAGAGAGAGCAAAAGAACAAAGAGA 282

QY      1167 ATGATCAAGAGAAAGCCCGAGACTGTTGGAAGCGAAGTGAAGCACTGAACCTCCAGG 1226
DB      283  AGAAGAGGAGAAAGCCCAAGAACTGTTGGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 342

QY      1227 TGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACTCAGCGAAGCTGAGCTAA 1286
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Db	875	TAAGGAGCTTCAAGAGGCTCAGCAAACTCAGTGAAGCTGAGCTCATGAAGAAGAGACT	816
QY	1300	TCAAGAAAGTGTGAGGCTTGAAGGAAATTTCTGCAATTCATCAGAGTTGAATGA	1359
Db	815	TCAAGAAATGTGAGGCTTGAAGGAAATTTCTGCAATTCATCAGAGTTGAATGA	756
QY	1360	AAAGCAAGAGCTTTTATTACTAAACAAAAGTTAGAGCTACAAAGTGAAGCATGCTATC	1419
Db	755	AAAGCAAGAGCTTTTATTATTAACAAAAGTTGAGCTTCAAGTGAAGCATGAGATC	696
QY	1420	AGAAATCAAAATGGACAGGCTTAAACACAGAGGATGAAAAGTCCAAATTAACCTGCTACA	1479
Db	695	AGAAATTAATGGAGCAAGGCTTAAACACAGAGGATGAAAAGTCCAAATTAACCTGCTACA	636
QY	1480	GATGACACACAAAGCTTCTTCAAGAACATTAATGCAATTTGAAAACAAATGAGAACT	1539
Db	635	GTTGACCCCAACAGGCTTCTTCAAGAAATCAATTAATGCAATTTGAAAACAAATGAGAACT	576
QY	1540	AAACAAAAGAGTGCAGAAAAGTGCACAGGCGAGTCTGGAAGGAAGTCAAGTGAAGAACT	1599
Db	575	GAAAGAGAGAGTCTGAAAAGTGGATAAGTGGTCTGCAGGAAGTCAATTTGAAGAGCT	516
QY	1600	GGAAGTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAC	1659
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QY	1720	TTACTGTTCTGATTTTTCATGCTGAAAGAGCAGCGAGAGAGAAATTCATGAGGAAAGGA	1779
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QY	1780	GCAACTGGCAATTCAGCTGGCAGTTCTGCTGAAAGAGAAATGATGCTTTCCAGAGCGAG-	1838
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QY	1897	CAGAGGCTTACTTGTTCAGAGAGGAGTGAAGGAGGAGTGGCGGCAACAG-----	1951
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QY	2011	GTTACAGATTCAGGATGATGATCATTTTAAGTGTGATGATGATGATGATGATGATGATGAT	2070
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QY	2071	TGTTGGT 2077	
Db	35	TGTTGGT 29	

RESULT 49	BU626293	693 bp	mRNA	linear	EST 23-SEP-2002
LOCUS	UI-H-DF0-bet-h-21-0-UI.s1	NCI CGAP DF0	Homo sapiens	cDNA clone	
DEFINITION	UI-H-DF0-bet-h-21-0-UI 3', mRNA sequence.				
ACCESSION	BU626293				
VERSION	BU626293.1	GI:23292508			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 693)				
AUTHORS	NCI-CGAP	http://www.ncbi.nlm.nih.gov/ncicgap.			
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Dr. Jose Mercuende cDNA Library preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu Seq primer: M13 FORWARD POLYA=Yes.	Location/Qualifiers 1..693 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="UI-H-DF0-bet-h-21-0-UI" /tissue_type="Subchondral Bone" /dev_stage="Adult" /lab_host="DH10B (Life Technologies)" /clone_lib="NCI CGAP DF0" /note="Organ: Bone; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP DF0 is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC. TAG TISSUE=Subchondral bone TAG_LIB=UI-H-DF0 TAG_SEQ=GTTAAGCGTC"	Query Match Best Local Similarity 31.0%; Score 643; DB 3; Length 693; Matches 654; Conservative 99.8%; Pred. No. 5.4e-155; 0; Mismatches 0; Indels 1; Gaps 1;		
QY	1423	AATCAAAATGGAACAGGCTTAAACACAGAGATGAAAAGTCCAAATTAACCTGTGCTACAGAT	1482		
Db	693	AATCAAAATGGAACAGGCTTAAACACAGAGATGAAAAGTCCAAATTAACCTGTGCTACAGAT	634		
QY	1483	GACACACACAGCTTCTTCAAGAACATAATTAATGCAATGAAAACAAATGAGGAACCTAAC	1542		
Db	633	GACACACACAGCTTCTTCAAGAACATAATTAATGCAATGAAAACAAATGAGGAACCTAAC	575		
QY	1543	AAAGAAAAGAGTCAGAAAAAGTGGACAGGCGAGTGTGGAAGGAACCTGAGTGAAAACTGGA	1602		
Db	574	AAAGAAAAGAGTCAGAAAAAGTGGACAGGCGAGTGTGGAAGGAACCTGAGTGAAAACTGGA	515		
QY	1603	ACTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCAATGGATGAAATGAAGCAACCAAT	1662		

Db 514 ACTGGCAGAGAGGCTCGCTTCAAAACAGCTGCAAAATGATGAATGAAGCAAAACCAT 455  
QY TGCCCAAGCAGAGAGGAGGACCTTGGAAACCATGACCATCTCAGGCTCAGATGGAAGTTTA 1722  
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Db 394 CTGTTCTGATTTTTCATCTGAAAGAGCAGGAGAGAGAAATTCATGAGGAAAGAGCA 335  
QY 1783 ACTGGCATTGACGTCGCTTCTGAAAGAGATGATCTTCAAGACGGAGCAG 1842  
Db 334 ACTGGCATTGACGTCGCTTCTGAAAGAGATGATCTTCAAGACGGAGCAG 275  
QY 1843 GCAGTCTTGTATGAGAGTGCATGATGGGGGAGAGCAAGTGAATCTGACACGCA 1902  
Db 274 GCAGTCTTGTATGAGAGTGCATGATGGGGGAGAGCAAGTGAATCTGACACGCA 215  
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Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-x@mail.nih.gov](mailto:cgapbs-x@mail.nih.gov)  
Tissue Procurement: Dr. James R. Lupski  
cDNA Library Preparation: Life Technologies, Inc.  
DNA sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
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GenCore version 5.1.8  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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ALIGNMENTS

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; APPLICANT: Williams, Lewis T.
; APPLICANT: Escobedo, Jaime
; APPLICANT: Innis, Michael A.
; APPLICANT: Garcia, Pablo Dominiguez
; APPLICANT: Sudduth-Klinger, Julie
; APPLICANT: Reinhard, Christoph
; APPLICANT: Giese, Klaus
; APPLICANT: Randazzo, Filippo
; APPLICANT: Kennedy, Giulia C.

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; APPLICANT: Kaskan, Altaf
; APPLICANT: Lamson, George
; APPLICANT: Drmanac, Radoje
; APPLICANT: Crkvenjakov, Radomir
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; APPLICANT: Drmanac, Snezana
; APPLICANT: Labat, Ivan
; APPLICANT: Leeshkowitz, Dena
; APPLICANT: Kita, David
; APPLICANT: Garcia, Veronica
; APPLICANT: Jones, William Lee
; APPLICANT: Stache-Crain, Birjit
; TITLE OF INVENTION: No. 6964868el Human Genes and Gene Expression
; FILE REFERENCE: 2300-1481
; CURRENT APPLICATION NUMBER: US/09/297,648
; CURRENT FILING DATE: 2000-03-10
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; PRIOR APPLICATION NUMBER: 60/075,954
; PRIOR FILING DATE: 1998-02-24
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; PRIOR APPLICATION NUMBER: 60/080,114
; PRIOR FILING DATE: 1998-03-31
; PRIOR APPLICATION NUMBER: 60/105,234
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US-09-297-648-4781

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COMPOSITIONS, KIT & METHOD FOR TREATMENT  
OF AIRWAY DISORDERS ASSOCIATED WITH  
BRONCHOCONSTRICTION, LUNG INFLAMMATION,  
NUMBER OF SEQUENCES: 3111  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.  
STREET: 7 Clarke Drive  
CITY: Cranbury  
STATE: NJ  
COUNTRY: USA  
ZIP: 08512  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-R  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: N/A  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: 60/127,958  
FILING DATE: 13-Apr-2000  
CLASSIFICATION: UNKNOWN  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/127,958  
FILING DATE: 1998-08-03  
ATTORNEY/AGENT INFORMATION:  
NAME: Amzel, Viviana  
REGISTRATION NUMBER: 30,930  
REFERENCE/DOCKET NUMBER: EPI-0067191b  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 609-409-3035  
TELEFAX: 413-254-9245  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 2716:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1994 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 2716

Query Match 3.7%; Score 76.6; DB 5; Length 1994;  
Best Local Similarity 57.2%; Pred. No. 8.3e-11;  
Matches 139; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 1576 GCTGAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTTGGCTTCCAAACAGCT 1635  
DB 925 GCTGGAAGATCTCAACAGCAGCTCCAGAGGCGGAGGAGGCTTGGTGGCCAAACAGGA 984  
QY 1636 GCAAAATGGATGAATGAAGCAAAACCAATTGCAAGCAGAGAGGACCTGGAAACCATGAC 1695  
DB 985 GGTGATCGATAAGCTGAAGGAGGAGGCGGAGCAGCAAGATTGTGATGAGACCGTTCC 1044  
QY 1696 CATCTCAGGGCTCAGATGAAGTTTACTTCTGATTTTCATGCTGAAAGAGCAGCGAG 1755  
DB 1045 GGTGCTGAAGGCCCGGCGGATATCTACAAGGCGGACTTCCAGGCTGAGAGGCGGCCG 1104  
QY 1756 AGAGAAATTCATGAGGAAAGGAGCAACTGGCATTGCGACTGCGCTTCTGCTGAAAGA 1815  
DB 1105 GGAGAGCTGGCGAGAGAGAGAGGAGCTCTGCGAGGAGCAGCTGGAGCAGCTGCAGAGGGA 1164  
QY 1816 GAA 1818  
DB 1165 GTA 1167

RESULT 8  
US-09-646-403-1  
; Sequence 1, Application US/09646403  
; Patent No. 6734174  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: KOVALENKO, Andrei  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR

; TITLE OF INVENTION: AND OTHER PROTEINS  
; FILE REFERENCE: WALLACH-27  
; CURRENT APPLICATION NUMBER: US/09/646,403  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: IL 123758  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: PCT/IL99/00158  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: IL 126024  
; PRIOR FILING DATE: 1998-09-01  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 2009  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-646-403-1

Query Match 3.7%; Score 76.6; DB 3; Length 2009;  
Best Local Similarity 57.2%; Pred. No. 8.3e-11;  
Matches 139; Conservative 0; Mismatches 104; Indels 0; Gaps 0;  
QY 1576 GCTGAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGGCTTGGCTTCCAAACAGCT 1635  
DB 930 GCTGGAAGATCTCAACAGCAGCTCCAGAGGCGGAGGAGGCTTGGTGGCCAAACAGGA 989  
QY 1636 GCAAAATGGATGAATGAAGCAAAACCAATTGCAAGCAGAGAGGACCTGGAAACCATGAC 1695  
DB 990 GGTGATCGATAAGCTGAAGGAGGAGGCGGAGCAGCAAGATTGTGATGAGACCGTTCC 1049  
QY 1696 CATCTCAGGGCTCAGATGAAGTTTACTTCTGATTTTCATGCTGAAAGAGCAGCGAG 1755  
DB 1050 GGTGCTGAAGGCCCGGCGGATATCTACAAGGCGGACTTCCAGGCTGAGAGGCGGCCG 1109  
QY 1756 AGAGAAATTCATGAGGAAAGGAGCAACTGGCATTGCGACTGCGCTTCTGCTGAAAGA 1815  
DB 1110 GGAGAGCTGGCGGAGAGAGAGGAGCTCTGCGAGGAGCAGCTGGAGCAGCTGCAGAGGGA 1169  
QY 1816 GAA 1818  
DB 1170 GTA 1172

RESULT 9  
US-09-646-403-2  
; Sequence 2, Application US/09646403  
; Patent No. 6734174  
; GENERAL INFORMATION:  
; APPLICANT: KOVALENKO, Andrei  
; APPLICANT: WALLACH, David  
; TITLE OF INVENTION: MODULATORS OF THE FUNCTION OF RECEPTORS OF THE TNF/NGF RECEPTOR  
; FILE REFERENCE: WALLACH-27  
; CURRENT APPLICATION NUMBER: US/09/646,403  
; CURRENT FILING DATE: 2000-09-18  
; PRIOR APPLICATION NUMBER: IL 123758  
; PRIOR FILING DATE: 1998-03-19  
; PRIOR APPLICATION NUMBER: PCT/IL99/00158  
; PRIOR FILING DATE: 1999-03-18  
; PRIOR APPLICATION NUMBER: IL 126024  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 2034  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-646-403-2

Query Match 3.7%; Score 76.6; DB 3; Length 2034;  
Best Local Similarity 57.2%; Pred. No. 8.4e-11;  
Matches 139; Conservative 0; Mismatches 104; Indels 0; Gaps 0;



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Db      7802 GTA 7804

RESULT 12
US-09-270-767-1308
; Sequence 1308, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1308
; LENGTH: 1827
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-1308

Query Match      2.4%; Score 49.8; DB 3; Length 1827;
Best Local Similarity 44.1%; Pred. No. 0.0027;
Matches 258; Conservative 0; Mismatches 322; Indels 5; Gaps 1;

QY 1104 AAAAGAAAACAAGTAATCGTTCTGAGATTGAAACCCACAGACAGAGGGGAGCAGACAGAGAAG 1163
Db 1241 AAGAGAAAAGAGAAGAGATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1300
QY 1164 AGAATGATGAAGAGAAAGGCCCGGAGACTGTTGGAAGCGAAGTGGAAAGCACTGAACCTCC 1223
Db 1301 AAGAGAAAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1360
QY 1224 AGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAACTCAGCGAAGCTGAGC 1283
Db 1361 AAGAGAAAAGAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1420
QY 1284 TAATGAAGAAGAGACTTCAAGAAAAGTGTTCAGGCCCTTGAAGAGAAAATTTCTCAATTC 1343
Db 1421 GAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1480
QY 1344 CATCAGAGTTGAATGAAAGCAAGAGCTTCTTTTACTACTACAAAGCTTAGAGCTACAAG 1403
Db 1481 GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1540
QY 1404 TGAAGACATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAAAGTCCA 1463
Db 1541 AAGAA-----GAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1595
QY 1464 AATTAAGTGTGTACAGATGACACAAAGCTTCTTCAAGAACATATAATGCAATTGA 1523
Db 1596 AGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1655
QY 1524 AAACAATTGAGGAACCTAACAGAAAAGAGTCAAGAAAAGTGGACAGGCGAGTCTGAAGG 1583
Db 1656 AGAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1715
QY 1584 AACTGAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGCAATGG 1643
Db 1716 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1775
QY 1644 ATGAATGAAGCAAACTTCCCAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1688
Db 1776 AAGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1820

RESULT 14
US-08-929-329-1
; Sequence 1, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmidium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
```

```
/ COUNTRY: USA
/ ZIP: 46204
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/929,329
/ FILING DATE:
/ CLASSIFICATION: 424
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Breen, John P
/ REGISTRATION NUMBER: 38,833
/ REFERENCE/DOCKET NUMBER: 835910-28685
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (317) 231-7745
/ TELEFAX: (317) 231-7433
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5433 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Plasmodium yoelii
/ US-08-929-329-1

Query Match 2.3%; Score 46.8; DB 3; Length 5433;
Best Local Similarity 44.1%; Pred. No. 0.035;
Matches 195; Conservative 0; Mismatches 247; Indels 0; Gaps 0;

QY 1198 AACGGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGC 1257
Db 3409 ACGTGAAGAAGCTGCAAGAAATCTGAGATAATAAGAAAATTTGAAGAAGCACAAGAGC 3468
QY 1258 TCATACAAACTCAGCGAAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTGAGC 1317
Db 3469 TCGGTGGGCAAAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3528
QY 1318 CCTTGAAGAGAAAATTTCTGCAATTCATCAGAGTTTGAATGAAAGCAAGAGCTTCTTTA 1377
Db 3529 GAGGAGAGAGAAACGAAATGAACTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3588
QY 1378 TACTAACAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCATGAAATCAAAATGGAACA 1437
Db 3589 AGCTGAAAAGAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3648
QY 1438 GGTAAACAGAGGATGAAAAGTCCAAATTAATCTGTGCTACAGATGACACACAAAGCT 1497
Db 3649 GGAAGAGAAAATTAATTGAAGCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3708
QY 1498 TCTTCAAGACATAATAATTCATTTGAAACCAATTTGAGGAACTAAACAGAGAGAGT 1557
Db 3709 AGCTAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3768
QY 1558 AAAAGTGGACAGGCGAGTGTGTAAGGAAGTGAAGTGAAGAACTGGAAGTGAAGAGAGGC 1617
Db 3769 AAGAAAAGAGGCTGAAGCTGTAAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3828
QY 1618 TCTGGCTTCCAAACAGCTGCAA 1639
Db 3829 AAGAAGAAAGCATGGAAGCTGAAA 3850

RESULT 15
US-09-902-540-1318
; Sequence 1318, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:

/ APPLICANT: Goldman, Barry S.
/ APPLICANT: Hinkle, Gregory J.
/ APPLICANT: Slater, Steven C.
/ APPLICANT: Wiegand, Roger C.
/ TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
/ FILE REFERENCE: 38-10(15849)B
/ CURRENT APPLICATION NUMBER: US/09/902,540
/ CURRENT FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: 60/217,883
/ PRIOR FILING DATE: 2000-07-10
/ NUMBER OF SEQ ID NOS: 16825
/ SEQ ID NO 1318
/ TYPE: DNA
/ ORGANISM: Myxococcus xanthus
/ FEATURE:
/ NAME/KEY: unsure
/ LOCATION: (1)..(614)
/ OTHER INFORMATION: unsure at all n locations
US-09-902-540-1318

Query Match 2.2%; Score 46.4; DB 3; Length 614;
Best Local Similarity 45.8%; Pred. No. 0.014;
Matches 193; Conservative 0; Mismatches 227; Indels 1; Gaps 1;

QY 1149 GCGACACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTGTGAAGCGAAGTGG 1208
Db 30 GTAAAAAAGAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAA 89
QY 1209 AAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAAAC 1268
Db 90 AAAAAATAATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 149
QY 1269 TCAGCGAAGCTCAGCTAATGAAGAGAGAGACTTCAAGAAAAGTGTCAAGGCCCTTGAAGGA 1328
Db 150 TGAGAAAACGAAAATATAGATAAAAAACAATAATAAAAAAAGAAAAAAGAAAAAAGAAAAA 209
QY 1329 AAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTGTGTTTATCTAACAACAA 1388
Db 210 AAAAAAGAGAAAAAACAACAACAAGAAAAAGCCGAATAAAAAAACAATAACACAATA 269
QY 1389 AGTTAGAGCTACAAGTGGAAAGCA-TGCTATCAGAAATCAAAATGGAACAGGCTAAAAACA 1447
Db 270 AACACAAAAAAGAACCAAAAAACAACAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 329
QY 1448 GAGGATGAAAGCTCCAAATTTAATCTGCTACAGATGACACACAAAGCTTCTTCAAGAA 1507
Db 330 ACAAAACAAAAACAAATAAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAG 389
QY 1508 CATAATAATGCAATTTGAAAAACAATTTGAGGAACTTAACAAGAAAAAGAGTCAGAAAAAGTGGAC 1567
Db 390 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 449
QY 1568 A 1568
Db 450 A 450

RESULT 16
US-09-949-016-3860
; Sequence 3860, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: CL001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
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; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3860
; LENGTH: 2719
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3860

```

Query Match	2.2%;	Score 46.2;	DB 3;	Length 2719;
Best Local Similarity	43.5%;	Pred. No. 0.035;		
Matches 210;	Conservative 0;	Mismatches 273;	Indels 0;	Gaps 0;
Qy	1170	ATGAAGAGAAGGCCGGAGACTGTTTGGAGCGAAGTGGAGGACACTGAACTCCAGGTGA	1229	
Db	848	ATMAAGTTTCAAGCACTCCCAACCMAAGGCATAGAGAACAAAGCTTTTGTATCGCAATACAG	907	
Qy	1230	CATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGCTGAGCTAATGA	1289	
Db	908	AATCTCTCTTTGAAGAACTGCTTCACCTGGCTCAGGCCCTAATAGGAGATGTGGATGAAG	967	
Qy	1290	AGAAGAGACTTCAAGAAAAGTGTGAGGCCCTTGAAAGGAAAAATCTTGCAAATTCCTATCAG	1349	
Db	968	GAGCAGATTTACTAGGAATGGTCCGGAAGTTGAGAATCTTATATTAGAAAAATACACAAC	1027	
Qy	1350	AGTTGATGAAAGCAGAGACTTGTTTTATCTACTACAAAAGTTAGAGCTACAGTGGAAA	1409	
Db	1028	TGTTGGAAAACCAAAATGCTTTGAAACATAGTGAAGATGATTTGTATAGCAAAAGTGGATG	1087	
Qy	1410	GCATGCTATCAGAAAATCAAAATGGAAACAGCGCTAAAACAGAGGATGAAAAGTCCAAATTAA	1469	
Db	1088	AAC TGACCTGTGAGAAGATGTGCTGCAAGGGNAATTGGAGGCTGTGNAACGAGCCAAAC	1147	
Qy	1470	CTGTGCTACAGATGACACACAACAAGTCTTTCAGAGAACATAATAATGCTATGAAAACAA	1529	
Db	1148	TGAAACTAGAGGAAAAGAACAGAGAATTGGAGGAAGAGCTTTAGAAAAGCTCGCGCAGAAG	1207	
Qy	1530	TTGAGGAACTAACAGAAAGAGTCTGAAAAAGTGGACAGGCGAGTCTCTGAAAGAACTGA	1589	
Db	1208	CTGAAGATGCAAGGCAAAAAAGCAAAAGATGACCATGATGTGATATTTCCACAGGCCGAGA	1267	
Qy	1590	GTGAAAAACTGGAACCTGGCAGAGAAGGCTCTGGCTTCCAAACAGCTGCCAAATGGATGAAA	1649	
Db	1268	GGAAACGGTTTACTAGAGTAGAATAGGCCCGTGTCTCATGGAGCGNAACCATGTATAG	1327	
Qy	1650	TGA	1652	
Db	1328	AGA	1330	

```

RESULT 17
US-09-710-279-693
; Sequence 693, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 693
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-693

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Query Match	2.2%; Score 46; DB 3; Length 627;
Best Local Similarity	46.3%; Pred. No. 0.018;
Matches 228; Conservative	0; Mismatches 255; Indels 9; Gaps 2;
Qy	1071 TCAAGGAGGCCAAGAAAGAGTTTTCAGATTTTGGAAAGAAACAAAGTAATCGTTCTGAGA 1130
Db	131 TTAATCAAGTAAGTAAAAAATAAAGCAATTAGAGAGAAAGCAAAATTTATTTAAAA 190
Qy	1131 TTGAAACCCAGACAGAGGGGAGACAGAGAAAGAGAAATGATGTAAGAGAAAGGCCCGGAGA 1190
Db	191 AGGTAATGATTAAGATCAAAGCACACGTTAAAGAAAGCAGCTGAAGATATA-----GTTGA 245
Qy	1191 CTGTTGAAGCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAGGAGCTTC 1250
Db	246 AATGTAAACAAGACAAAAGAAATTTGAAAAGAGAGAGGCTCTAGATAATTTCTGA 305
Qy	1251 AAGAGGCTCATACAAAACCTCAGCGAAGCTCAGCTAATGAAAGAGAGACTTCAAGAAAAAGT 1310
Db	306 AAAAGCATTTAAACAAGCCAAAGCAATATCTTGAACATGTAGAAACA----AAGCAAAGA 361
Qy	1311 GTCAGGCCCTTGAAGAGAAAAATCTTGCAATTCATCAGAGTTGAATGAAAAGCAAGAGC 1370
Db	362 AAAAGAAGTTGAACAACTTGATAGTGCTATTAAAGAAAAATATAATCATCATGATGCTT 421
Qy	1371 TTGTTTATCTAACAAAAAGTTAGAGCTCAAGTGGAAAGCATGCTATCAGAATCAAAA 1430
Db	422 ATGCAAGGCTTACAAAAAGCACTTAATAAGGAAAAAGAACTGTTTCTTTATTGATG 481
Qy	1431 TGGAAACAGGCTAAAAACAGAGGATGAAAGTCCAAATTAACGTGCTACAGATCACACACA 1490
Db	482 AAGTAAATGCAACAAATCGAAGTAGACGGAATAATCGAAAGATCTTTCTAAAGCATATA 541
Qy	1491 ACAAGCTTCTTCAAGAACATAATAATGCAATGAGTAAAAACAATGAGGAACTTAACAAAGAAAG 1550
Db	542 AAGAAATGAATAATAAATTTAATGCTTACTCAAAAGCCATTGAGAAAGTAAAAAAGAGAAA 601
Qy	1551 AGTCAGAAAAAG 1562
Db	602 AACAAATGTAG 613
RESULT 18	
US-09-710-279-1325	
; Sequence 1325, Application US/09710279	
; Patent No. 6703492	
; GENERAL INFORMATION:	
; APPLICANT: KIMWERY, WILLIAM JOHN	
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS	
; FILE REFERENCE: PU34800S	
; CURRENT APPLICATION NUMBER: US/09/710,279	
; CURRENT FILING DATE: 2000-11-09	
; PRIOR APPLICATION NUMBER: 60/164,258	
; PRIOR FILING DATE: 1999-11-09	
; NUMBER OF SEQ ID NOS: 4472	
; SOFTWARE: PatentIn ver. 2.1	
; SEQ ID NO 1325	
; LENGTH: 627	
; TYPE: DNA	
; ORGANISM: Artificial Sequence	
; FEATURE:	
; OTHER INFORMATION: Description of Artificial Sequence: synthetic	
; OTHER INFORMATION: nucleic acid sequence	
US-09-710-279-1325	

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RESULT 18
US-09-710-279-1325
; Sequence 1325, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1325
; LENGTH: 627
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-1325

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	Query Match	Best Local Similarity	2.2%;	Score 46;	DB 3;	Length 627;
	Matches 228;	Conservative	46.3%;	Pred No. 0;	0.018;	
				Mismatches 255;	Indels 9;	Gaps 2;
Qy	1071	TCAAGGAGGCCAAGAAAGAGTTTCAGATTTTCAAAAGAAAAACAAGTAATCGTTCGAGA				1130
Db	131	TTAATCAAGTAAGTAAAAAATAAACAAGATTACAGAGAAAGCAAAATATTATTAAAA				190

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QY 1131 TTGAACCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGATGAAGAAAGGCCCGGAGA 1190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 191 AGTAAATGATAAAGATCAAGCAGACAGTAAAGAAAGCAGCTGAAGATATA-----GTTGA 245
QY 1191 CTGTTGAAGCGAAGTGAAGAGCACTGAACTCTCAGGTGACATCTCTGTTTAAAGGAGCTTC 1250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 246 AAATGTAAACAAAGACAAAGAAATTTGAAAAGAGAGAGAGGCTCTAGATAATTTCTGA 305
QY 1251 AAGAGGCTCATACAAACTCAGCGAGCTGAGCTAATGAGAGAGAGACTTCAGAAAAGT 1310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 306 AAAAGCATTTAAACAAGCCAGCAATATCTTGAACATGTAGAAAACA-----AAGCAAGA 361
QY 1311 GTCAGGCCCTTGAAGGAAAAATTTCTGCAATTCATCAGAGTTCATGAAAGAAAGCAAGAGC 1370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 362 AAAAGAGTTGAACAACTTGATAGTGTCTATTAAAGAAAATATAATCATATGTCCT 421
QY 1371 TTGTTTATATACAAAGATTAGAGCTACAACTGGAAGCATGCTATCAGAAATCAAAA 1430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 422 ATCAAGGCTTACAAAAAGCACTTAATAAGGAAAAAGAACTGTTTCTTATTGAAATG 481
QY 1431 TGGACAGGCTAAACAGAGATGAAAGTCCAAATTAATTAAGTCTACAGATGACACACA 1490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 482 AAGATAATGCAACAACTCGGAAGTAGCGGAAAAATCGAAAGATCTTTCTAAAGCATATA 541
QY 1491 ACAAGCTTCTTCAAGAACATAATAATGCATTGAAAACAATTTGAGAACTAAACAAGAAAAG 1550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 542 AAGAAATGAATAATAATTAATGCTTACTCAAAAGCCATTGAGAAAGTAAAGAGAGAA 601
QY 1551 AGTCAGAAAAAG 1562
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 602 AACAGATGTAG 613

RESULT 19
US-09-134-001C-578
; Sequence 578, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 578
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-578

Query Match 2.2%; Score 46; DB 3; Length 633;
Best Local Similarity 46.3%; Pred. No. 0.018;
Matches 228; Conservative 0; Mismatches 255; Indels 9; Gaps 2;

QY 1071 TCAAGGAGGCCAAAGAAAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGA 1130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 137 TTAATCAAGTAAGTAAAAAATAAACGAATTAGAAGAGAAAAAGCAAAAAATTTATTAATA 196
QY 1131 TTGAACCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAGAAAGGCCCGGAGA 1190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 197 AGSTAAATGATAAAGATCAAAGCAGACAGCTAAAAAAGCAGCTGAAGATATA-----GTTGA 251
QY 1191 CTGTTGAAGCGAAGTGAAGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTC 1250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 252 AAATGTAAACAAAGACAAAAGNAATTTGAAAAGAGAGAGAGGCTCTAGATAATTTCTGA 311
QY 1251 AAGAGGCTCATACAAAATCTCAGGGAAGCTGAGCTAATGAAAGAGAGACTTCAAGAAAAGT 1310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 312 AAAAGAAATTTAAACAAGCCAGCAATATCTTGAACATGTAGAAAAACA-----AAGCAAGA 367
QY 1311 GTCAGGCCCTTGAAGGAAAAATTTCTGCAATTCCTCATCAGAGTTGAATGAAAAGCAAGAGC 1370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 AAAAAGAAAGTTGAACAACCTTGATAGTGTCTATTAAAGAAAAATATAAATCATATGTCCT 427
QY 1371 TTGTTTATACTAACAAAAAGTTAGAGCTACAAAGTGAAGAGCATGCTATCAGAAATCAAAA 1430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 428 ATGCAAGGCTTACAAAAAGACACTTAATAAGGAAAAAGAACTGTTTCTTATTGAAATG 487
QY 1431 TGAACAGGCTAAACAGAGGATGAAAGTCCAAATTAATTAAGTCTGCTACAGATGACACACA 1490
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 488 AAGATAATCAACACAATCGGAAGTAGACGGAATAATCGAAAGATCTTTCTTAAAGCATATA 547
QY 1491 ACAAGCTTCTTCAAGAACATAATAATGCATTGAAAACAATTTGAGAACTAAACAAGAAAAG 1550
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 548 AAGAAATGAATAATAATTAATGCTTACTCAAAAGCCATTGAGAAAGTAAAGAGAGAA 607
QY 1551 AGTCAGAAAAAG 1562
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 608 AACAGATGTAG 619

RESULT 20
US-09-710-279-4039/c
; Sequence 4039, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4039
; LENGTH: 2999
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
US-09-710-279-4039

Query Match 2.2%; Score 46; DB 3; Length 2999;
Best Local Similarity 46.3%; Pred. No. 0.042;
Matches 228; Conservative 0; Mismatches 255; Indels 9; Gaps 2;

QY 1071 TCAAGGAGGCCAAAGAAAGTTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGA 1130
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1689 TTAATCAAGTAAGTAAAAAATAAACGAATTTAGAGAGAAAAAGCAAAAAATTTATTTAAAA 1630
QY 1131 TTGAACCCAGACAGAGGGGAGCAGAGAAAGAGAAATGATGAGAAAGGCCCGGAGA 1190
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1629 AGSTAAATGATAAAGATCAAAGCAGACAGCTAAAAAAGCAGCTGAAGATATA-----GTTGA 1575
QY 1191 CTGTTGAAGCGAAGTGAAGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTC 1250
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1574 AAATGTAAAAACAAGACAAAAAGAAATTTGAAAAGAGAGAGAGGCTCTAGATAATTTCTGA 1515
QY 1251 AAGAGGCTCATACAAACTCAGCGAAGCTGAGCTAATGAAAGAGAGACTTCAAGAAAAGT 1310
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1514 AAAGCATTTAAACAAGCCAGCAATATCTTGAACATGTAGAAAAACA-----AAGCAAGA 1459
QY 1311 GTCAGGCCCTTGAAGGAAAAATTTCTGCAATTCATCCATCAGAGTTGAATGAAAAGCAAGAGC 1370
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1458 AAAAAGAAAGTTGAACAACCTTGATAGTGTCTATTAAAGAAAAATATAAATCATATGTCCT 1399
QY 1371 TTGTTTATACTACAAAAGTTAGAGCTACAAAGTGAAGAGCATGCTATCAGAAATCAAAA 1430
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1398 ATCAAGGCTTACAAAAAGCACTTAATAAGGAAAAAGAACTGTTTCTTATTGTAATG 1399
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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QY 1431 TGGACAGGCTAAACACAGAGATGAAAGTCCAAATTAACCTGTCTACAGATGACACACA 1490  
Db 1338 AAGATAATGCAACACAATCGGAAGTAGACGGAAATCGAAGATCTTTCTAAAGCATATA 1279  
QY 1491 ACAAGCTCTTCAAGAACATTAATGATGATGAAACAAATGAGGAACATAACAGAAAG 1550  
Db 1278 AAGAAATGAATTAATTAATTTAATGCTTACTCAAAAGCCATTGAGAAAGTAAAGAGAAA 1219  
QY 1551 AGTCAGAAAAAG 1562  
Db 1218 AACAGATGTAG 1207  
RESULT 21  
US-09-710-279-3338/c  
; Sequence 3338, Application US/09710279  
; Patent No. 6703492  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/09/710,279  
; PRIOR FILING DATE: 2000-11-09  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 258  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3338  
; LENGTH: 3691  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: nucleic acid sequence  
US-09-710-279-3338

Query Match 2.2%; Score 46; DB 3; Length 3691;  
Best Local Similarity 46.3%; Pred. No. 0.047;  
Matches 228; Conservative 0; Mismatches 255; Indels 9; Gaps 2;  
QY 1071 TCAAGGAGCCAAAGAAAGAGTTTCAGATTTTGAAGAAAGAAACAAAGTAATCTGTCTGAGA 1130  
Db 2729 TTAATCAAGTAAGTAAAGAAATAAACAAGATTTAGAGAGAAAGAAACAAAGAAATTTATTTAAA 2670  
QY 1131 TTGAACCCACAGAGGGGACACAGAGAAAGAGATGTGAAGAGAAAGGCCCGGAGA 1190  
Db 2669 AGGTAATGATAAGATCAAGACACACGTAAAGAAAGCAGCTGAAGATATA-----GTTGA 2615  
QY 1191 CTGTTGGAAGCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTC 1250  
Db 2614 AAATGTAACAAAGACAAAAGAAATTTGAAGAAAGAGAGAGGCTCTAGTAATTTCTGA 2555  
QY 1251 AAGAGGCTCATACAAAACCTCAGCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAGT 1310  
Db 2554 AAAAGCATTTAAACAAGCCAAAGCAATATCTTGAACATGTAGAAAACA-----AAGCAAGA 2499  
QY 1311 GTCAGGCCCTGAAGGAAAATTTCTGCAATTTCCATCAGATTTGAATGAAGAAAGCAAGC 1370  
Db 2498 AAAAAGAAAGTTGAACAACCTTGATAGTGTATTTAAAGAAAAATATAATCATCATGATGCTT 2439  
QY 1371 TTGTTTATCTAACAAAAGGTTAGAGCTTACAAGTGGAAAGCATCTCTATCAGAAATCAAAA 1430  
Db 2438 ATGCAAGGCTTACAAAAGACACTTAATAGGAAAAGAACTGTTTCTTTATTTGATG 2379  
QY 1431 TGGAAACAGGCTAAACACAGAGATGAAAGTCCAAATTAACCTGTCTACAGATGACACACA 1490  
Db 2378 AAGATAATGCAACACAATCGGAAGTAGACGGAAATCGAAAGATCTTTCTAAAGCATATA 2319  
QY 1491 ACAAGCTTCTCAGAACATTAATGCAATGAAACAAATTTGAGAACTTAACAGAAAG 1550  
Db 2318 AAGAAATGAATAATAATTAATGCTTACTCAAAAGCCATTGAGAAAGTAAAGAGAAA 2259

QY 1551 AGTCAGAAAAAG 1562  
Db 2258 AACAGATGTAG 2247  
RESULT 22  
US-09-270-767-5061  
; Sequence 5061, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5061  
; LENGTH: 705  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-5061  
Query Match 2.2%; Score 45.2; DB 3; Length 705;  
Best Local Similarity 45.7%; Pred. No. 0.032;  
Matches 235; Conservative 0; Mismatches 273; Indels 6; Gaps 2;  
QY 1103 GAAAGAGAAACAGTAATCGTTCTGAGATTGAAACCCACAGACAGAGGGGACACAGAGAAA 1162  
Db 135 GGAAGAGGACAAAGAGAGAGAGAGAGGAAAGAGAGAGGAAAGAGGAAAGAGAG 194  
QY 1163 GAGAATGATCAAGAGAAAGCCCGGAGACTGTTGGAAAGCGAAGTGGAGCACTGAACCTC 1222  
Db 195 AGAAGAGAAAGAAAGAGAGAGAGGGGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAA 254  
QY 1223 CAGGTGACATCTCTGTTTAAAGAGACTTCAAGAGGCTCATACAAACTCAGCGAAGCTGAG 1282  
Db 255 GAGGAAAGAGAGAGAGAGAGAGGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 314  
QY 1283 CTATGAGAGAGAGACTTCAAGAAAGAGTGTCCAGGCCCTTGAAGGAAAAATTCGCAATT 1342  
Db 315 AGAAAG 374  
QY 1343 CCATCAGAGTTGAATGAAGCAAGAGACTGTTTATATACTAACAAAAAGTTAGAGCTACAA 1402  
Db 375 AG 434  
QY 1403 GTGGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAAGTCC 1462  
Db 435 GAGGAAAAAG 492  
QY 1463 AAATTAACCTGTCTACAGATGACACACAAAGCTTCTTCAAGACATATAATGCAATTG 1522  
Db 493 AG 548  
QY 1523 AAAACAATTCAGGAACTTAACAGAAAAAGAGTCAGAAAAAGTGCAGAGGCGAGTCTCAAG 1582  
Db 549 AAAAG 608  
QY 1583 GAATCAGTGAAAACTGGAACTTGGCAAGTGGCAGAGAGAG 1616  
Db 609 AAAGAGACAG 642  
RESULT 23  
US-09-270-767-20343  
; Sequence 20343, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767

; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 20343  
; LENGTH: 705  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-20343

Query Match 2.2%; Score 45.2; DB 3; Length 705;  
Best Local Similarity 45.7%; Pred. No. 0.032;  
Matches 235; Conservative 0; Mismatches 273; Indels 6; Gaps 2;  
  
QY 1103 GAAAGAAAACAGTAATCGTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAGAAA 1162  
DB 135 GGAAGAGACACAGAGAGAGGAGGGAAGGACGAGAGAGAGGGAAGAAAGAG 194  
  
QY 1163 GAGAATGATCAAGAGAAAGCCCGGAGACTGTTGGAGCGAAGTGGAACTGGAACCTC 1222  
DB 195 AGAAGAGAAAGAAAGAGAGAGGGGAAAGAGGAGGAGGAAAGAAAGAGGAA 254  
  
QY 1223 CAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATCAAACTCAGCGAGCTGAG 1282  
DB 255 GAGGAAAGAAAGAGAGAGAGGAGGAAAGAAAGAGGAGGAGGAGGAG 314  
  
QY 1283 CTAATCAAGAGAGAGACTTCAAGAAAAGTGTGAGGCCCTTGAAGGAGAAAATTCGCAATT 1342  
DB 315 AGAAAAGAGAGAGGAGAAAAGAAAAGAGAGGAGAGAAAAGAGAGGAAAGAA 374  
  
QY 1343 CCATCAGAGTTGAATGAAAGCAAGAGCTGTTTATTACTAAACAAAAGTTAGAGCTACAA 1402  
DB 375 AGAGAGAGGAGAAAAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 434  
  
QY 1403 GTGGAAGCATGCTATCAGAAATCAAAATGGAACAGCGCTTAAACAGAGATGAAAGTCC 1462  
DB 435 GAGGAAAAAGAAAAGAGAGAGAGAGAA--AAAGAGAGAGGAGGAGGAGGAGGAGGAG 492  
  
QY 1463 AAATTAACGTGCTCAGAGATGACACACAAAGCTTCTTCAAGAAATATTAATGATG 1522  
DB 493 AGAAAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 548  
  
QY 1523 AAAACAATTGAGAACTAACAGAAAAGAGTCAAGAAAAGTGGACAGGCGAGTGTGAAG 1582  
DB 549 AAAAGAAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 608  
  
QY 1583 GAACTGAGTCAAAACTGGACTGGCAGAGAGG 1616  
DB 609 AAAGAGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 642

RESULT 24  
US-09-461-697-193  
; Sequence 193, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 193  
; LENGTH: 696  
; TYPE: DNA

; ORGANISM: Homo sapiens  
US-09-461-697-193

Query Match 2.1%; Score 44.6; DB 3; Length 696;  
Best Local Similarity 43.5%; Pred. No. 0.047;  
Matches 203; Conservative 0; Mismatches 264; Indels 0; Gaps 0;  
  
QY 1212 CACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCA 1271  
DB 171 CACAGAAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 230  
  
QY 1272 GCGAAGCTGAGCTAATGAGAGAGACTTCAAGAAAAGTGTTCAGGCCCTTTGAAAGGAAAA 1331  
DB 231 AGATCAGAAAAGAGATGAAGAGATCAAAAACGAGAGAAAGGGGAGCTGGAAAAGAGA 290  
  
QY 1332 ATTCTGCAATCCATCAGAGTTGAATGAAAAGCAAGAGCTTGTATTATCTACAAAAGCT 1391  
DB 291 CAAAGATGAAAAGGGGAGAGATGGAAAAGAGGATAAAAATGGAATGAGAAAGGAGA 350  
  
QY 1392 TAGAGCTCAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAAAACAGAGG 1451  
DB 351 AGATGCAAAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 410  
  
QY 1452 ATGAAAAGTCCAAATTAATCTGTGTACAGATCACACACAAAGCTTCTTCAAGAACATA 1511  
DB 411 TGGAAAAGAGAAAGGAGAGATGAAAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 470  
  
QY 1512 ATAATGCATTGAAAACATTTGAGGAACCTAACAGAAAAGAGTCAGAAAAGTGGACAGG 1571  
DB 471 AAAAGAGATGAAGATGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 530  
  
QY 1572 CAGTGTCAAGGAACTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1631  
DB 531 CAAAAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 590  
  
QY 1632 AGCTGCAATGATGAATGAAGCAACCATTTGCCAAGCAGGAAGAG 1678  
DB 591 AGCTGMAAGAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 637

RESULT 25  
US-09-461-697-191  
; Sequence 191, Application US/09461697  
; Patent No. 6277974  
; GENERAL INFORMATION:  
; APPLICANT: COGENT NEUROSCIENCE, Inc.  
; APPLICANT: Lo, Donald C.  
; APPLICANT: Barney, Shawn  
; APPLICANT: Thomas, Mary Beth  
; APPLICANT: Portbury, Stuart D.  
; APPLICANT: Purnam, Kasturi  
; APPLICANT: Katz, Lawrence C.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING  
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING  
; FILE REFERENCE: 10001-005-999  
; CURRENT APPLICATION NUMBER: US/09/461,697  
; CURRENT FILING DATE: 1999-12-14  
; NUMBER OF SEQ ID NOS: 466  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 191  
; LENGTH: 699  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-461-697-191

Query Match 2.1%; Score 44.6; DB 3; Length 699;  
Best Local Similarity 43.5%; Pred. No. 0.047;  
Matches 203; Conservative 0; Mismatches 264; Indels 0; Gaps 0;  
  
QY 1212 CACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATACAAAACCTCA 1271  
DB 174 CACAGAAAAGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 233

```
QY 1272 GCGAAGCTGACTTAATGAAGAGAGACTTCAAGAAAAAGTGTGAGGCCCTTGAAGGAAAA 1331
Db 234 AGATCAGAAAAAGATGAAGAAGATCAAAACGAAGAGAGAGGGAAGCTGGAAGAAGA 293
QY 1332 ATTCTGCAATTCATCAGAGTTGAATGAAGAAGAGAGCTGTTTATCTACAAACAAAGT 1391
Db 294 CAAGATGAAAAAGGGGAAGAGATGGAAGAAAGAGGATAAAAATGGAATGAGAAAGGAGA 353
QY 1392 TAGAGCTACAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGAGCTAAAAACAGAGG 1451
Db 354 AGATGCAAAAGAGAAAGAGATGGAAGAAAGAGTGAAGACGGAAGAAAGGAATGAGAGAGA 413
QY 1452 ATGAAAGTCCAAATTAAGTGTCTACAGATGACACAAACAAAGCTTCTTCAAGAACATA 1511
Db 414 TGGAAAGAGAGAGAGAGATGAAAAAGAGGAAAGACACAGAAAGAAAAACAGGAGTTGG 473
QY 1512 ATRATGATTCAGAAACAATTGAGCACTTAACAGAAAGAGTTCAGAAAAAGTTCAGAAAAAGTGCACAGG 1571
Db 474 AAAAGAGATGAAGATGGAAGAGAGAGGAGATAAAAAGAGAGGGAAGGGAAGATGTAAAAAGT 533
QY 1572 CAGTGTGAAGGAATGAGTGAAGAAAGTGAAGCTGGCAGAGAAAGGCTCTGGCTTCCAAAC 1631
Db 534 CAAGAGATGAAAAAGAGAGAGAGATGGAAGAAAGAGATGAAGTGAAGTGAAGAGAGA 593
QY 1632 AGCTGCAAAATGGAATGAAGCAAAACCAATTGCAAGCAGGAAAGAG 1678
Db 594 AGCTGGAAGAGAGAAAGAGATTTAAAAAGAGAGAGGAAAGGAAAAAG 640
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## RESULT 26

```
US-09-461-697-189
; Sequence 189, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 717
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-189
```

```
Query Match 2.1%; Score 44.6; DB 3; Length 717;
Best Local Similarity 43.5%; Pred. No. 0.047;
Matches 203; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
```

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QY 1212 CACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATCAAAACTCA 1271
Db 192 CACAGAAAAGGAGGAGAAAAAGAAAGAGCAGTGGCAGCAGAGTAAAAATGAAGAAGA 251
QY 1272 GCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTGAGGCCCTTGAAGGAAAA 1331
Db 252 AGATCAGAAAAGAGATGAAGAAGATCAAAACGAGAGAGAAAGGGAAGCTGGAAGAAGA 311
QY 1332 ATTCTGCAATTCATCAGAGTTGAATGAAGAAGAGAGCTGTTTATCTACAAACAAAGT 1391
Db 312 CAAGATGAAAAAGGGAAGAGATGGAAGAAAGAGGATAAAAATGGAATGAGAAAGGAGA 371
QY 1392 TAGAGCTACAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAAAACAGAGG 1451
```

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Db 372 AGATGCAAAAGAGAGAAAGATGGAAGAAAAAGGTGAAGACGGAAGAAAGAAATGGAAGA 431
QY 1452 ATGAAAGTCCAAATTAAGTGTCTACAGATGACACAAACAAAGCTTCTTCAAGAACATA 1511
Db 432 TGGAAAGAGAGAGGAGAGATGAAAAAGAGGAAAGACAGAGAAAGAAACAGGAGTTGG 491
QY 1512 ATRATGATTCAGAAACAATTGAGGAACTTAACAGAAAGAGTTCAGAAAAAGTTCAGAAAAAGTGCACAGG 1571
Db 492 AAAAGAGATGAAGATGGAAGAAAGAGAGAGGAGATAAAAAGAGGGAAGAGATGTAAAAAGT 551
QY 1572 CAGTGTGAAGGAAGTGAAGTGAAGAACTGGCACTGGCAGAGAGAGGCTCTGGCTTCCAAAC 1631
Db 552 CAAGAGAGATGAAAAAGAGAGAGAGATGGAAGAAAGAGATCAAGGTGGAATGAGGAAGA 611
QY 1632 AGCTGCAAAATGGAATGAAGCAAAACCAATTGCAAGCAGGAAAGAG 1678
Db 612 AGCTGGAAGAGAGAAAGAGATTTAAAAAGAGAGGAAAGGAAAAAG 658
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## RESULT 27

```
US-09-461-697-189
; Sequence 187, Application US/09461697
; Patent No. 6277974
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Portbury, Stuart D.
; APPLICANT: Puranam, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; FILE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-999
; CURRENT APPLICATION NUMBER: US/09/461,697
; CURRENT FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-461-697-187
```

```
Query Match 2.1%; Score 44.6; DB 3; Length 774;
Best Local Similarity 43.5%; Pred. No. 0.049;
Matches 203; Conservative 0; Mismatches 264; Indels 0; Gaps 0;
```

```
QY 1212 CACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATCAAAACTCA 1271
Db 249 CACAGAAAAGGAGGAGAAAAAGAAAGACGATGGAAGAGAGAGGGAAGCTGGAAGAAGA 308
QY 1272 GCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTGAGGCCCTTGAAGGAAAA 1331
Db 309 AGATCAGAAAAGAGATGAAGAAGATCAAAACGAGAGAGAAAGGGAAGCTGGAAGAAGA 368
QY 1332 ATTCTGCAATTCATCAGAGTTGAATGAAGAAGCAAGAGCTGTTTATCTACAAACAAAGT 1391
Db 369 CAAGATGAAAAAGGGAAGAGATGGAAGAAAGAGGATAAAAATGGAATGAGAAAGGAGA 428
QY 1392 TAGAGCTACAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAAAACAGAGG 1451
Db 429 AGATGCAAAAGAGAAAGAGATGGAAGAAAGAGTGAAGACGGAAGAAAGAAATGGAAGA 488
QY 1452 ATGAAAGTCCAAATTAAGTGTCTACAGATGACACAAACAAAGCTTCTTCAAGAACATA 1511
Db 489 TGGAAAGAGAGAGAGAGATCAAAAGAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGTGG 548
QY 1512 ATRATGATTCAGAAACAATTGAGGAACTTAACAGAAAGAGAGTTCAGAAAAAGTTCAGAAAAAGTGCACAGG 1571
Db 549 AAAAGAGATGAAGATGGAAGAAAGAGAGAGGAGATAAAAAGAGGGAAGAGATGTAAAAAGT 608
```



APPLICANT: Treacy, Maurice  
APPLICANT: Spaulding, Vikki  
APPLICANT: Agostino, Michael J.  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
TITLE OF INVENTION: SECRETED THEM  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/993,228  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Sprunger, Suzanne A.  
REGISTRATION NUMBER: 41,323  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 498-8284  
TELEFAX: (617) 876-5851  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3113 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-993-228-20

Query Match 2.1%; Score 44.6; DB 2; Length 3113;  
Best Local Similarity 43.3%; Pred. No. 0.11;  
Matches 209; Conservative 0; Mismatches 274; Indels 0; Gaps 0;  
QY 1170 ATGAGAGAAAGCCCGAGACTGTTGGAAGCGAAGTGGAGCACTGAACTCCAGTGA 1229  
DB 139 ATAAGGTTCAAGCACTCCCAACCAAGGCATAGAGACAAAGCTTTTGATCGCAATACAG 198  
QY 1230 CATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAAACTCAGCGAAGCTGAGCTAATGA 1289  
DB 199 AATCTCTTTGAAGAACTGTTCTCAGCTGGCTCAGGCCCTAATAGGAGATGTGGATGAAG 258  
QY 1290 AGAAGAGACTTCAAGAAAAGTGTGAGCCCTTGAAGGAAAAAATTTCTGCAATTCCTAATCAG 1349  
DB 259 GAGCAGATTTTACTAGGAATGGGTGGGAAGTTGAGAACTTTATATTAGAAAAATACACAAC 318  
QY 1350 AGTTGAATGAAGCAAGAGCTGTTTATTACTAACAAGAAAGTTAGAGCTACAGTGGAAA 1409  
DB 319 TGTGGAAACCAAAAATGCTTTGAACATAGTGAAGAAATGATTTGATAGCAAAAGTGGATG 378  
QY 1410 GCATGCTATCAGAAATCAAAATGGAACAGAGCTTAAACAGAGGATGAAAGTCCCAATTA 1469  
DB 379 AACTGACCTGTGAGAAAGATGTGCTGCAAGGGAAATTTGGAGGCTGTGAAAGCAAGCCAAAC 438  
QY 1470 CTGTGCTACAGATGACACAAACAAGCTTCTTCAAGAACATAATAATGCAATTTGAAAAACAA 1529  
DB 439 TGAACCTAGAGGAAAAAGAACAGAGAAATTTGGAGGAGAGCTTAGGAAAGCTCGGCAGAG 498  
QY 1530 TTGAGGAACTAACAGAAAAGAGTCAAGAAAAGTGGACAGGCAAGTCTCAAGAACTGA 1589  
DB 499 CTGAAGATGCGGGCAAAAAGCAAAAGATGACCATGATGATGATTTCCCAACAGCCACAGA 558  
QY 1590 GTGAAAACCTGGAAGTGGCAGAGAGGCTCTGGCTTCCAACAGAGCTCAATGGATGAAA 1649  
DB 559 GGAACCGTTTACTAGAGTAGAAATGGCCCGTGTCTCATGGAGCGCAACCAAGTATTAAG 618

QY 1650 TGA 1652  
DB 619 AGA 621

## RESULT 31

US-09-902-540-1357  
; Sequence 1357, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1357  
; LENGTH: 612  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; NAME/KEY: unsure  
; LOCATION: (1)..(612)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1357

Query Match 2.1%; Score 44.4; DB 3; Length 612;  
Best Local Similarity 43.1%; Pred. No. 0.049;  
Matches 207; Conservative 0; Mismatches 273; Indels 0; Gaps 0;  
QY 1082 AAAGAAAGCTTTCAGATTTTGAAGAAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCAG 1141  
DB 26 AA 85  
QY 1142 ACAGAGGGGACACAGAGAAAGAGATGATGAAGAGAAAGCCCGAGACTGTTGGAGC 1201  
DB 86 AA 145  
QY 1202 GAAGTGAAGCACTGAACCTCCAGGTCATCTCTGTTTAAAGGAGCTTCAAGAGGCTCAT 1261  
DB 146 AA 205  
QY 1262 ACAAACCTGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTGAGGCCCTT 1321  
DB 206 AA 265  
QY 1322 GAAGGAAAGAAATTTCTGCAATTTCCATCAGAGTTGAAATGAAAGCAAGAGCTTGTGTTTACT 1381  
DB 266 AA 325  
QY 1382 AAAAAAAAAAGTTAGAGCTTACAAAGTGAAGCATGCTATCAGAAATCAAAATGGAACAGCT 1441  
DB 326 AA 385  
QY 1442 AAAAAAGAGAGTGAAGAGTCCAAATTAATGCTGTGCTACAGATGACACAAACAGCTTCTT 1501  
DB 386 AATATATAAATAA 445  
QY 1502 CAGAACATAATATGCAATTTGAACAATTTGAGAGACTTACAGAAAAGAGTCAAGAAAA 1561  
DB 446 AAAAAAAAAATAATAA 505

## RESULT 32

US-09-248-796A-6172  
; Sequence 6172, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:



APPLICANT: Keith Weinstock et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
FILE REFERENCE: 107196.132  
CURRENT APPLICATION NUMBER: US/09/248,796A  
CURRENT FILING DATE: 1999-02-12  
PRIOR APPLICATION NUMBER: US 60/074,725  
PRIOR FILING DATE: 1998-02-13  
PRIOR APPLICATION NUMBER: US 60/096,409  
PRIOR FILING DATE: 1998-08-13  
NUMBER OF SEQ ID NOS: 28208  
SEQ ID NO 6172  
LENGTH: 1893  
TYPE: DNA  
ORGANISM: Candida albicans  
US-09-248-796A-6172

Query Match 2.1%; Score 44.4; DB 3; Length 1893;  
Best Local Similarity 44.2%; Pred. No. 0.092;  
Matches 183; Conservative 0; Mismatches 231; Indels 0; Gaps 0;

QY 1053 AGAGACTTGAGTGGACCTCAAGAGGCCCAAGAAAGAGTTTCAGATTTTGAAGAAAA 1112  
DB 1283 AGAAATTTGAATATATTTGATTAGTGAAGAAAAAGAAAAAAGTGAACAAAGAACTTGA 1342  
QY 1113 CAAGTAATCTGCTGAGATTGAAACCCAGACAGAGGGGAGCAGAGAGAAAGAAATGATG 1172  
DB 1343 CAAACACACGCTGAACCTTGAAAACTGATTGATGATTAATAATGCTGATCCAGTAAGA 1402  
QY 1173 AAGAGAAAGCCCGGAGACTGTGGAAGCGAAGTGAAGCACTGAACTCCAGGTGACAT 1232  
DB 1403 CAAATTCGTGATCTTGAAAAAGCCCAACAAGAAAGTATTGGACCTTGAAACGCACTTGA 1462  
QY 1233 CTCCTGTTAAGGAGCTTCAGAGGCTCATACAAAACCTCAGCGAGCTGAGCTTAATGA 1292  
DB 1463 AACTTACCAGAACTTGATTAATAAATCTGGAATTTACAAAACATGAAAAATTTGAACA 1522  
QY 1293 AGAGACTTCAAGAAAAGTGTGAGCCCTTGAAAGGAAAAATCTGCAATTTCCATCAGAGT 1352  
DB 1523 ATGAATTCACCAATTTGAGTAATATCATGAGAAATTTAACTAAATTAGACAAAATTG 1582  
QY 1353 TGAATGAAAGCAAGAGCTGTGTTTATCTAAACAAAAAGTTAGAGCTACAAGTGGAAAGCA 1412  
DB 1583 AAAATGAAAGAAATGATCTTGTCAAATCATCATGAAAACTCAATGTTGAACATAAGAAA 1642  
QY 1413 TGCATCAGAAATCAAAAATGGAACAGGCTTAAACAGAGGATGAAAAGTCCAAAT 1466  
DB 1643 CGTCAACAAAATTTACAAAATGTTTGAAGAGAAAAATAAGAAAAATCAGAGCAAAAT 1696

RESULT 33  
US-09-270-767-8286/c  
Sequence 8286, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 8286  
LENGTH: 851  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: n means any nucleotide  
US-09-270-767-8286

Query Match 2.1%; Score 44; DB 3; Length 851;  
Best Local Similarity 44.6%; Pred. No. 0.077;  
Matches 262; Conservative 0; Mismatches 320; Indels 6; Gaps 2;

QY 1031 AGGGAAGGAATCAGAAGTGGAGAGA-CTTGAAGTTGCACCTCAAGGAGCCCAAGAAAG 1089  
DB 757 AGGGGAGAGAAAAAGAAAGAGAGAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 698  
QY 1090 AGTTTCAGATTTTGAAGAAAGAAAGTAAATCGTTCTGAGATTGAAACCCAGACAGAGG 1149  
DB 697 AAGTAGAGAAAAAGGAGAAAGAAAGAGAGAGAAAAAGAAAGAAAGAAAGAGGAGAGGA 638  
QY 1150 GAGCACAGAAAGAGAAATGATGAAGAGAAAGCCCGGAGACTGTTTGGAGCGCAAGTGA 1209  
DB 637 AAGAAAAAGGAAAGGGGAAAGGAAAGAAAGAAAGAAAGAAAGAAAGGAGAGAGAGAA 578  
QY 1210 AGCACTGAACTCCAGGTCACATCTCTGTTTAAAGAGCTTCAAGAGGCTTCATACAAAACT 1269  
DB 577 GAAAGGGAGAGGAGAAAGAAAGAGGAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 518  
QY 1270 CAGCGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAAGTGTCAAGGCCCTTGAAG--- 1326  
DB 517 GAGGGAAGAAAGAAAGAAAGAGAGAAAAATATAGAAAAAGAAAGAAAGAAAGATGAAGGG 458  
QY 1327 --GAAAAATTCGCAATTCATCAGATTCCTGAGTTGAAATGAAACCAAGAGCTTCTTTATACTAAC 1384  
DB 457 GAGAAAGAGGAAAGAGAGAAAAAGAGGGGAAAGAAAGAAAGAGAAAGAGGAAAGAAAG 398  
QY 1385 AAAAAAGTTAGAGCTTACAAGTGAAGAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAA 1444  
DB 397 AAGGAGAAAGAAAGAAAGAAATCAAGAAAGAGGAGGAGAGAGAAAGAAAGAAAGGGGG 338  
QY 1445 ACAGAGGATGAAAGTCCAAATTAATGTTGCTACAGATGACACACAAAGCTTCTTCAA 1504  
DB 337 AGAAAAAGAAAGAGGGGAGGAAAGAGAAAGAGGAAAAAGAAAGAAAGAGAGAGAGAAA 278  
QY 1505 GAACATATATGCTATTGAAACAATTGAGGAACTTAACAGAAAAAGAGTCAGAAAAAGTG 1564  
DB 277 AGAGAGGAAAGAAAGAGGGGAAAAAGAAAGGGGAGAAAAAGAAAGAAAGAAAGAGAGAA 218  
QY 1565 GACAGGGCAGTCTGAAGGAACTGAGTGAAGAACTGGAACCTGGAACCTGGCAGAG 1612  
DB 217 GGAAGGGAGGGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 170

RESULT 34  
US-09-270-767-23568/c  
Sequence 23568, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 23568  
LENGTH: 851  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
FEATURE:  
OTHER INFORMATION: n means any nucleotide  
US-09-270-767-23568

Query Match 2.1%; Score 44; DB 3; Length 851;  
Best Local Similarity 44.6%; Pred. No. 0.077;  
Matches 262; Conservative 0; Mismatches 320; Indels 6; Gaps 2;  
QY 1031 AGGGAAGGAATCAGAAGTGGAGAGA-CTTGAAGTTGCACCTCAAGGAGCCCAAGAAAG 1089  
DB 757 AGGGGAGAGAAAAAGAAAGAGAGAGAAAGGAAAGGAAAGAAAGAAAGAAAGAAAGAA 698  
QY 1090 AGTTTCAGATTTTGAAGAAAGAAAGTAAATCGTTCTGAGATTGAAACCCAGACAGAGG 1149  
DB 697 AAGTAGAGAAAAAGGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAGGAGAGGA 638



```
US-09-949-016-77355
; Sequence 77355, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 77355
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-77355
```

```
Query Match      2.1%; Score 43.6; DB 3; Length 601;
Best Local Similarity 48.7%; Pred. No. 0.082;
Matches 115; Conservative 1; Mismatches 120; Indels 0; Gaps 0;

QY 1328 AAAAAATTCGCAATCCATCAGAGTTGAATGAAAAAGCAGAGCTGTTTATATCAACAAA 1387
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1388 AAGTTAGAGCTCAAGTGGAAACATGCTATCAGAAATCAAAATGGAACAGGCTAAACA 1447
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1448 GAGGATGAAAGTCCAAATTAATGCTACAGATGACACACAAACAGCTTCTTCAAGAA 1507
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1508 CATAATAATGCAATGAGAACTAACAAGAAAAAGCAGTCAAGAAAAGT 1563
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1563 CAGGAATATTAATACCAAGAAATGACCAACAGACGCGCACAAAAAAGACAGAAAAAT 1660
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

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RESULT 38
US-09-949-016-16602/c
; Sequence 16602, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16602
; LENGTH: 55841
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16602
```

```
Query Match      2.1%; Score 43.6; DB 3; Length 55841;
Best Local Similarity 46.0%; Pred. No. 0.99;
Matches 148; Conservative 0; Mismatches 174; Indels 0; Gaps 0;
```

```
QY 1276 AGCTGAGCTAATGAAGAAGAGAGCTTCAAGAAAAGTGTGAGGCCCTTTGAAAGGAAAAATTC 1335
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1336 TGCATTCATCAGAGTTGAATGAAAAAGCAGAGCTGTTTATATCAACAAAAAGTTAGA 1395
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1396 GCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACACAGAGATCA 1455
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1456 AAAAGTCCAAATTAATGCTACAGATGACACACAAACAGCTTCTTCAAGAAACATAATAA 1515
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1516 TGCATTTGAAAAAATTTGAGGAATTAACAAAGAAAAAGAGTCAGAAAAAGTGGACAGGCGAT 1575
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1576 GCTGAAGGAAGTGAAGTGAAGAA 1597
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1600 AAGAAAGGAGAAAGAGAGAAAGAA 1625
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

```
RESULT 39
US-09-336-115C-23
; Sequence 23, Application US/09336115C
; Patent No. 6576244
; GENERAL INFORMATION:
; APPLICANT: Weltzin, Richard A.
; APPLICANT: Guy, Bruno
; TITLE OF INVENTION: LT and CT in Parenteral Immunization
; TITLE OF INVENTION: Methods Against Helicobacter Infection
; FILE REFERENCE: 06132/055002
; CURRENT APPLICATION NUMBER: US/09/336,115C
; CURRENT FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: US 09/100,258
; PRIOR FILING DATE: 1998-06-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 1149
; TYPE: DNA
; ORGANISM: Helicobacter pylori
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (106)...(1002)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (106)...(166)
US-09-336-115C-23
```

```
Query Match      2.1%; Score 43.4; DB 3; Length 1149;
Best Local Similarity 46.3%; Pred. No. 0.13;
Matches 143; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 1081 CAAAGAAGAGTTTCAGATTTTGAAGAAACAGATTAATCGTTCTGAGATTGAACCCCA 1140
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 GACAGAGGGGACACAGAGAAAGAGATGATCAAGAGAAAGCCCGGAGACTGTTTGAAG 1200
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1201 CGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCA 1260
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1261 TACAAACTCAGCGAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAGTGTGAGGCCCT 1320
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1320 TAAAGAAACAGGCTTTAGTGAATTTTGGCTTAAAGAAAGAGGCTGAAGAAAGTGAAGAAAGT 1380
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 211 GATGGTGGAGAAACACAGGAAGAGCCCAAGGTTGAGGCGAGAGAAAAAGCGAGACAA 270  
Qy 1157 GAGAAAGAGAAATGATGAAGAGAAAGCCCGGAGAGCTGTTGGAAGCGAGTGAAGCACTG 1216  
Db 271 GAGCGAGAAAGAGCGAGAGAAAGAGCGAGAGAAAGAGCGAGAGCGAGAGAA 330  
Qy 1217 AACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAAACTCAGCGA 1275  
Db 331 GAGGCTCCGCTGAGTCCGCAAGAGAGACTACAAACACATTGCTACTCTCTCATCGA 389

RESULT 45

US-10-04-047-1957  
; Sequence 1957, Application US/10104047  
; Patent No. 6943241  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: No. 6943241el full length cDNA  
; FILE REFERENCE: HI-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; PRIOR FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1957  
; LENGTH: 1685  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-04-047-1957

Query Match 2.1%; Score 42.8; DB 3; Length 1685;  
Best Local Similarity 44.2%; Pred. No. 0.24;  
Matches 176; Conservative 0; Mismatches 222; Indels 0; Gaps 0;  
Qy 1281 AGCTAATGAAGAAGAGACTTCAAGAAAGTGTACAGCCCTTGAAGAGAAATTTCTGCAA 1340  
Db 721 AGAAGATGAAGAAGATCAAAACGAAGAGAAAGGGGAAGCTGGAAAGAGACAAAGATGA 780  
Qy 1341 TTCCATCAGAGTTGAATGAAGCAAGAGCTGTTTATCTACTAACAAGAGTTAGAGCTAC 1400  
Db 781 AAAAGGGAAGAGATGGAAGAGAGGATATAAAATGGAATGGAAGAGGAGAGATGCAAA 840  
Qy 1401 AAGTGAAGAGATGCTACTCAGAAATCAAAATGGAACAGGCTTAAACAGAGGATGAAAGT 1460  
Db 841 AGAGAAAGAGATGGAAGAAAGAGTGAAGACGGAAGGAATGGAAGAGATGGAAGAA 900  
Qy 1461 CCAATTAATGCTGCTACAGATGACACACAAAGCTTCTTCAAGAACATAATAATGCAT 1520  
Db 901 GAAAGGAGAGATGMAAAGAGGAGAAAGACAGAAAGAAACAGGGGATGMAAAGAGAA 960  
Qy 1521 TGAACCAATGAGGAACTAACAGAAAGAGTCAAGAAAGTGAAGAGGAGGAGTGTGTA 1580  
Db 961 TGAAGATGGAAGAGAGAGAGGAGATATAAAGAGGGGAGAGATGTAAAGTCAAGAGAA 1020  
Qy 1581 AGCAACTGAGTGAAGAACTGGAATGCGCAGAGAGGCTCTGGCTTCCAAACAGCTGCAAA 1640  
Db 1021 TGAAGAGAGAGAGAGATGGAAGAGAGATGAAGATGAAGTGGAAATGAGGAGAGAGCTGGA 1080  
Qy 1641 TGGATGAATGAAGCAACCACTTTCGCAAGCAGGAAGAG 1678  
Db 1081 AGAGAAAGAGATTTAAAGAGAGAGGAGGAAGGAAGAG 1118

RESULT 46

US-09-614-221A-426  
; Sequence 426, Application US/09614221A  
; Patent No. 6723837  
; GENERAL INFORMATION:  
; APPLICANT: Karunanandaa, Balasulojini  
; APPLICANT: Yu, Jaehyuk  
; APPLICANT: Kishore, Ganesh M.

; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED  
; FILE REFERENCE: 16516.075  
; CURRENT APPLICATION NUMBER: US/09/614,221A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/142,981  
; PRIOR FILING DATE: 1999-07-12  
; NUMBER OF SEQ ID NOS: 626  
; SEQ ID NO 426  
; LENGTH: 345  
; TYPE: DNA  
; ORGANISM: Saccharomyces cerevisiae  
US-09-614-221A-426

Query Match 2.1%; Score 42.6; DB 3; Length 345;  
Best Local Similarity 47.5%; Pred. No. 0.12;  
Matches 126; Conservative 0; Mismatches 139; Indels 0; Gaps 0;  
Qy 1435 ACAGGCTAAACACAGAGGATGAAAGTCCAATTAACCTGTGCTACAGATGACACACAA 1494  
Db 33 ACAAGCTGAAAGGAGAGCCACGAAATAGTATCAAGGCTAGAAAGTACAGACAGATAA 92  
Qy 1495 GCTTCTTCAAGACATAATATGATTGAAACAAATGAGGAACCTAACAGAAAAGATC 1554  
Db 93 GTTGAAGCAAGCCCAAGACTGATGCGCAAGGAAATCGACTCATACAAAATTCAAAAAGA 152  
Qy 1555 AGAAAAAGTGACAGGCGAGTGTGAAAGAACTGAGTGAAAACTGGAACTGGCAGAGAA 1614  
Db 153 CAAGGAATTTGAAGAGTTTGAACAAAAGAAATGCCGGTGGTGGTGAATTTGGAAGAA 212  
Qy 1615 GGCTCTGGCTTCCAAACAGCTGCAATGGATGAAATGAAGCAAAACCACTTGCCAAAGCAGGA 1674  
Db 213 AGCAGAGGCTGTTGTCAGGTGAATTAGCTGAGATTGAAGAAATTCGAGAGAGAGAAAA 272  
Qy 1675 AGAGGACCTGGAACCATGACCATC 1699  
Db 273 GGATGACGTTGTCAAAAATTTTGATC 297

RESULT 47

US-09-902-540-1280  
; Sequence 1280, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Wiegand, Roger C.  
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof  
; FILE REFERENCE: 38-10(15849)B  
; CURRENT APPLICATION NUMBER: US/09/902,540  
; CURRENT FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: 60/217,883  
; PRIOR FILING DATE: 2000-07-10  
; NUMBER OF SEQ ID NOS: 16825  
; SEQ ID NO 1280  
; LENGTH: 1039  
; TYPE: DNA  
; ORGANISM: Myxococcus xanthus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(1039)  
; OTHER INFORMATION: unsure at all n locations  
US-09-902-540-1280

Query Match 2.1%; Score 42.6; DB 3; Length 1039;  
Best Local Similarity 51.0%; Pred. No. 0.21;  
Matches 99; Conservative 0; Mismatches 95; Indels 0; Gaps 0;  
Qy 1375 TTATCTAACAAAAAGTTAGAGCTACAGTGGAAAGCATGCTATCAGAAATCAAAATGGA 1434  
Db 380 TTAAAAATAAAAAATTAATTTACAAACAAATAAAAGAAAAAATRAAAAAAATAAATA 439

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QY 1435 ACAGGCTAAACAGAGGATGAAAAGTCCAAATTAACGTGCTACAGATGACACACAACAA 1494
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Db 440 ATATGTAAATAAATAAACAACAACAACACCAACCAACCAACCAACCAACCAACCAACCA 499
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QY 1495 GCTCTTCAAGAACATAATAATGTCATTTGAAACAATTTGAGGAAGCTTCAACGAAGAAAGAGTC 1554
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Db 500 ATCAAAACAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 559
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QY 1555 AGAAAAGTGGACA 1568
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RESULT 48
US-09-949-016-14000
; Sequence 14000, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14000
; LENGTH: 154626
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(154626)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14000
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Best Local Similarity 48.7%; Pred. No. 3.8;
Matches 115; Conservative 0; Mismatches 121; Indels 0; Gaps 0;

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Db 58226 AAGATATTTTGAAGTGTATATGAAGTGTATAAAGAGAAAAGAAAGGAATTGAAGGAAAAAG 58285
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QY 1388 AAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAAAACA 1447
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Db 58286 ACACCAAGAAAAAAGACAGCGCATTAATTTAAAGCTTCTGAAGAACTTCTAGAAATATA 59345
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QY 1448 GAGGATGAAAAGTCCAAATTAACGTGCTACAGATGACACACAACAGAGCTTCTTCAAGAA 1507
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Db 58346 GAACATTAAATTCACACATAAATGGTCTAACGGTTAAACAGCAGACTGAATTGAATTGA 59405
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QY 1508 CATAATAATGCATTTGAAAACAATTTGAGGAAGCTTAAACGAAGAAAAGAGTCAGAAAAAGT 1563
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Db 58406 CAGGAATATTTAACTACGAGAAATGAGCAACAGACGCAACAAAAAGACAGAAAAAT 58461
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RESULT 49
US-09-640-173-53/c
; Sequence 53, Application US/09640173
; Patent No. 6613515
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: OVARIAN TUMOR SEQUENCES AND
; METHODS OF USE THEREFOR
; FILE REFERENCE: 210121.484C2

Query Match 2.0%; Score 41.8; DB 3; Length 396;
Best Local Similarity 47.6%; Pred. No. 0.21;
Matches 109; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1333 TTCTGCAATTCATCAGAGTTGAATGAAAAGCAGAGCTTGTATTACTAACAAAAAGTT 1392
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Db 271 TTCTTTTCTTTTNTGAAATTAANAAGCNAAAAAANAANAANNTTAAAAAAGGAAAA 212
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QY 1393 AGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGA 1452
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Db 211 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 152
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QY 1453 TGAAGAATCCAAATTAACGTGCTACAGATGACACACAACAGCTTCTTCAAGAACATAA 1512
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; CURRENT APPLICATION NUMBER: US/09/640,173
; CURRENT FILING DATE: 2000-08-15
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-640-173-53

Query Match 2.0%; Score 41.8; DB 3; Length 396;
Best Local Similarity 47.6%; Pred. No. 0.21;
Matches 109; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1333 TTCTGCAATTCATCAGAGTTGAATGAAAAGCAGAGCTTGTATTACTAACAAAAAGTT 1392
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Db 211 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 152
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QY 1453 TGAAGAATCCAAATTAACGTGCTACAGATGACACACAACAGCTTCTTCAAGAACATAA 1512
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QY 1513 TAATGCATTGAAAACAATTTGAGGAAGCTTAAACGAAGAAAGAGTCAGAAAAA 1561
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Db 91 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 43
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RESULT 50
US-09-713-550-53/c
; Sequence 53, Application US/09713550
; Patent No. 6617109
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; THERAPY AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.484C4
; CURRENT APPLICATION NUMBER: US/09/713,550
; CURRENT FILING DATE: 2000-11-14
; NUMBER OF SEQ ID NOS: 205
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 396
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(396)
; OTHER INFORMATION: n = A,T,C or G
US-09-713-550-53
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Query Match 2.0%; Score 41.8; DB 3; Length 396;
Best Local Similarity 47.6%; Pred. No. 0.21;
Matches 109; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1333 TTCTGCAATTCATCAGAGTTGAATGAAAAGCAGAGCTTGTATTACTAACAAAAAGTT 1392
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Db 271 TTCTTTTCTTTTNTGAAATTAANAAGCNAAAAAANAANAANNTTAAAAAAGGAAAA 212
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QY 1393 AGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAGGA 1452
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Db 211 AAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAAAAGAAAA 152
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1453 TGAAGAATCCAAATTAACGTGCTACAGATGACACACAACAGCTTCTTCAAGAACATAA 1512
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Db 151 AA 92  
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Db 91 AA 43

Search completed: May 29, 2006, 11:34:03  
Job time : 673 secs

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C 93 49.8 2.4 600 10 US-10-972-079-13288 Sequence 13288, A
C 94 49.4 2.4 1155 8 US-10-221-714A-475 Sequence 475, App
C 95 49.2 2.4 446 3 US-09-960-352-3400 Sequence 3400, App
C 96 49.2 2.4 1297 9 US-10-425-115-126557 Sequence 126557,
C 97 49.2 2.4 9297 9 US-10-425-115-67687 Sequence 67687, A
C 98 48.8 2.3 629 7 US-10-125-968-78 Sequence 78, Appl
C 99 48.4 2.3 5142 6 US-10-097-340-42 Sequence 42, Appl
C 100 48.4 2.3 5142 13 US-11-050-926-42 Sequence 42, Appl
C 101 48 2.3 344 3 US-09-960-352-1036 Sequence 1036, App
C 102 48 2.3 447 8 US-10-021-323-9573 Sequence 9573, App
C 103 47.8 2.3 14006 7 US-10-311-455-1931 Sequence 1931, App
C 104 47.6 2.3 516 3 US-09-960-352-5785 Sequence 5785, App
C 105 47.4 2.3 6866 8 US-10-433-793-80 Sequence 80, Appl
C 106 47.4 2.3 6668 7 US-10-311-455-1670 Sequence 1670, App
C 107 47.2 2.3 468 9 US-10-674-124A-12575 Sequence 12575, A
C 108 47.2 2.3 1214 7 US-10-424-599-102083 Sequence 102083,
C 109 46.8 2.3 3913 7 US-10-233-045-12 Sequence 12, Appl
C 110 46.6 2.2 6171 7 US-10-311-455-761 Sequence 761, App
C 111 46.6 2.2 7571 7 US-10-311-455-500 Sequence 500, App
C 112 46.4 2.2 767 8 US-10-424-599-70401 Sequence 70401, A
C 113 46.4 2.2 1029 7 US-10-425-115-123086 Sequence 123086,
C 114 46.4 2.2 2418 7 US-10-369-493-23839 Sequence 23839, A
C 115 46.4 2.2 9539 6 US-10-239-676-52 Sequence 52, Appl
C 116 46.4 2.2 9539 7 US-10-240-453-54 Sequence 54, App
C 117 46.2 2.2 411 8 US-10-424-599-79490 Sequence 79490, A
C 118 46.2 2.2 899 7 US-10-369-493-29260 Sequence 29260, A
C 119 46.2 2.2 921 9 US-10-425-115-38710 Sequence 38710, A
C 120 46.2 2.2 1204 7 US-10-437-963-77858 Sequence 77858, A
C 121 46.2 2.2 2523 7 US-10-205-219-158 Sequence 158, App
C 122 46.2 2.2 3791 7 US-10-240-965-3 Sequence 3, Appli
C 123 46.2 2.2 3825 9 US-10-422-522-8 Sequence 8, Appli
C 124 46.2 2.2 4286 6 US-10-044-090-549 Sequence 549, App
C 125 46.2 2.2 6145 7 US-10-311-455-945 Sequence 945, App
C 126 46.2 2.2 3673778 7 US-10-312-841-2 Sequence 2, Appli
C 127 46.2 2.2 627 10 US-10-793-626-693 Sequence 693, App
C 128 46 2.2 627 10 US-10-793-626-1325 Sequence 1325, App
C 129 46 2.2 633 8 US-10-724-972A-1807 Sequence 1807, App
C 130 46 2.2 2999 10 US-10-793-626-4039 Sequence 4039, App
C 131 46 2.2 3691 10 US-10-793-626-3338 Sequence 3338, App
C 132 46 2.2 10170 16 US-11-136-527-1817 Sequence 1817, App
C 133 46 2.2 5625 9 US-10-723-860-7708 Sequence 7708, App
C 134 45.8 2.2 2350 7 US-10-602-494-302 Sequence 302, App
C 135 45.6 2.2 5750 8 US-10-221-714A-433 Sequence 433, App
C 136 45.6 2.2 6301 7 US-10-311-455-26 Sequence 26, Appl
C 137 45.6 2.2 484 9 US-10-425-115-172345 Sequence 172345,
C 138 45.4 2.2 809 9 US-10-363-345A-20409 Sequence 20409, A
C 139 45.4 2.2 809 9 US-10-363-345A-20410 Sequence 20410, A
C 140 45.4 2.2 809 10 US-10-363-483A-20409 Sequence 20409, A
C 141 45.4 2.2 809 10 US-10-363-483A-20410 Sequence 20410, A
C 142 45.4 2.2 868 8 US-10-437-963-42302 Sequence 42302, A
C 143 45.4 2.2 1016 8 US-10-424-599-13347 Sequence 1347, App
C 144 45.4 2.2 6010 9 US-10-723-860-57 Sequence 57, Appl
C 145 45.4 2.2 6010 9 US-10-723-860-105 Sequence 105, App
C 146 45.4 2.2 6010 9 US-10-723-860-4858 Sequence 4858, App
C 147 45.4 2.2 7442 8 US-10-221-714A-409 Sequence 409, App
C 148 45.4 2.2 17934 7 US-10-311-455-1692 Sequence 1692, App
C 149 45.4 2.2 17934 7 US-10-311-455-1692 Sequence 1692, App
C 150 45.4 2.2 17934 7 US-10-311-455-1692 Sequence 1692, App
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## ALIGNMENTS

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RESULT 1
US-10-609-133-1
; Sequence 1, Application US/10609133
; Publication No. US20040191798A1
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut Health Center
; APPLICANT: Sarfarazi, Mansoor
; APPLICANT: Rezaie, Tayebbeh
; APPLICANT: Child, Anne H
; TITLE OF INVENTION: Optineurin and Glaucoma
; FILE REFERENCE: UCT-0046P2
; CURRENT APPLICATION NUMBER: US/10/609,133
; PRIOR FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10,281,457
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 10,090,118
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 10,060,981
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/344,754
; PRIOR FILING DATE: 2001-12-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 2077
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Rezaie, T., Child, A., Hitchings, R., Brice, G., Miller, L.,
; AUTHORS: Coca-Prodos, M., Heon, E., Krupin, T., Ritch, R., Kreutzer, D.,
; AUTHORS: Crick, R.P., and Sarfarazi, M.
; TITLE: Adult-Onset Primary Open-Angle Glaucoma Caused by Mutations in
; TITLE: Optineurin
; JOURNAL: Science
; VOLUME: 295
; ISSUE: 5557
; PAGES: 1077-1079
; DATE: 2002
; DATABASE ACCESSION NUMBER: AF420371
; DATABASE ENTRY DATE: 2002-02-11
; RELEVANT RESIDUES: (1)..(2077)
US-10-609-133-1
Query Match 99.9%; Score 2075.4; DB 9; Length 2077;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2076; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 ATCCCGGTGGAGGTTCTCTCCAGGGGCGACGATCCGAGGAAACAGTACCTTGAGCGA 60
Db 1 ATCCCGGTGGAGGTTCTCTCCAGGGGCGACGATCCGAGGAAACAGTACCTTGAGCGA 60
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Db 121 TGAGCGGTACGCGCTCTGTAAACCCCACTTCCTCACCTTTGAAACAGCTGCTGGTTT 180
QY 181 ATTAATGAAGATTAGTCAGTGACGCGCTGGTGTGCTGATCGGACATAGAGATCAA 240
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Db 1501 TCAAGAACATAATATGCTTGAATTTGAAACAAATTTGAGGAACCTAACAGAAAGAGTCAAGAA 1560  
Qy 1561 AGTGGACAGGCGAGTCTGAGGAACTGAGTGAAGAACTGAGTGAAGAACTGAGTGAAGGCTCT 1620  
Db 1561 AGTGGACAGGCGAGTCTGAGGAACTGAGTGAAGAACTGAGTGAAGAACTGAGTGAAGGCTCT 1620

Qy 1621 GGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCATTCGCCAAGCAGGAAGAGGA 1680  
Db 1621 GGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCATTCGCCAAGCAGGAAGAGGA 1680  
Qy 1681 CTTGGAAACCATGACCAATCCTCAGGGCTCAGATGGAAGATTTACTGTCTGATTTTCATGC 1740  
Db 1681 CTTGGAAACCATGACCAATCCTCAGGGCTCAGATGGAAGATTTACTGTCTGATTTTCATGC 1740  
Qy 1741 TGAAGAGCAGCAGAGAGAGAAATTTATGAGGAAAGAGCAACTGGCATTGTCAGCTGGC 1800  
Db 1741 TGAAGAGCAGCAGAGAGAGAAATTTATGAGGAAAGAGCAACTGGCATTGTCAGCTGGC 1800  
Qy 1801 AGTTCTCTGAAAGAGAAATGATCTTTTGAAGAGCGAGGAGGAGCTTGTGATGGAGAT 1860  
Db 1801 AGTTCTCTGAAAGAGAAATGATCTTTTGAAGAGCGAGGAGGAGGAGCTTGTGATGGAGAT 1860  
Qy 1861 GCAGAGTCGTATGGGCGAGAAACAGTGAATCTGACAGAGGAGCTTACCTTGTTCAAAG 1920  
Db 1861 GCAGAGTCGTATGGGCGAGAAACAGTGAATCTGACAGAGGAGCTTACCTTGTTCAAAG 1920  
Qy 1921 AGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTTCCTCTGCCCAA 1980  
Db 1921 AGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTTCCTCTGCCCAA 1980  
Qy 1981 GTGTGGAGAGGTTCTGCTGACATAGACAGTTTACAGATTTCAGTGTGATTCATCAT 2040  
Db 1981 GTGTGGAGAGGTTCTGCTGACATAGACAGTTTACAGATTTCAGTGTGATTCATCAT 2040  
Qy 2041 TTAAGTGTGATGATGATACCTCCCAAACTGTTGGT 2077  
Db 2041 TTAAGTGTGATGATGATACCTCCCAAACTGTTGGT 2077

## RESULT 2

US-10-172-118-128  
; Sequence 128, Application US/10172118  
; Publication No. US20030224374A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Chris  
; APPLICANT: Van 't Veer, Laura  
; APPLICANT: Van de Vijver, Marc  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-175-999  
; CURRENT APPLICATION NUMBER: US/10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; PRIOR APPLICATION NUMBER: 60/380,770  
; PRIOR FILING DATE: 2002-05-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 128  
; LENGTH: 2139  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: AF061034  
; DATABASE ENTRY DATE: 2001-06-18  
US-10-172-118-128

Query Match 99.0%; Score 2056.4; DB 7; Length 2139;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2071; Conservative 0; Mismatches 6; Indels 1; Gaps 1;  
Qy 1 ATCCCGGTGGGAGTTCTCTCCAGGCGGACGATCGGAGAAACAGTACCTGACCGGA 60  
Db 16 ATCCCGGTGGGAGTTCTCTCCAGGCGGACGATCGGAGAAACAGTACCTGACCGGA 75  
Qy 61 AGCCAAAGCCGCGGAGGTGTGATAGCTGTGTGTCACCTTCTGCGCTTGGGA 120

Db 76 AGCCAAGCCGGCGGCGAGGTGTGGCTTTGATAGCTGGTGGTGCACCTTCTCGGCCTTGGA 135  
Qy 121 TGAGCGGTACGGCTCTGTAAACCCAACTTCCTCACTTTGAAACAGCTGCCTGTTTCAGC 180  
Db 136 TGAGCGGTACGGCTCTGTAAACCCAACTTCCTCACTTTGAAACAGCTGCCTGTTTCAGC 195  
Qy 181 ATTAAATGAAGATTAGTCAGTGACAGGCTGGTGTGCTGAGTCCGACATAGAGAATCAA 240  
Db 196 ATTAAATGAAGATTAGTCAGTGACAGGCTGGTGTGCTGAGTCCGACATAGAGAATCAA 255  
Qy 241 AAATGTCAAAATGTAACTGAGAGAAAGTGGCAACTTTT - GGAAGTGAATTTTTCACAG 299  
Db 256 AAATGTCAAAATGTAACTGAGAGAAAGTGGCAACTTTTGGGAGTGACTTTTTCACAG 315  
Qy 300 GAACTTCTCAATGTCCTCACTCACTCTCAGCTGCCTCACTGAAAGGAGGACAGCCCA 359  
Db 316 GAACTTCTCAATGTCCTCACTCACTCTCAGCTGCCTCACTGAAAGGAGGACAGCCCA 375  
Qy 360 GTGAAAGCAGGAAATGACCCGCCCACTGGCCCACTGGAACAGTGTACCC 419  
Db 376 GTGAAAGCAGGAAATGACCCGCCCACTGGCCCACTGGAACAGTGTACCC 435  
Qy 420 CGGAGAGCTGCTGCAGCAGATGAAGAGCTCTGACCAAGAACCACTGAGTGAAGAAG 479  
Db 436 CGGAGAGCTGCTGCAGCAGATGAAGAGCTCTGACCGAGAACCACTGAGTGAAGAAG 495  
Qy 480 CCATGAAGCTAAATTAATCAAGCCATGAAGGGAGATTGAGGAGCTTTTCGGCTTGACAG 539  
Db 496 CCATGAAGCTAAATTAATCAAGCCATGAAGGGAGATTGAGGAGCTTTTCGGCTTGACAG 555  
Qy 540 AGAAAACAGAAAGAAACCCAGTTTTTTTTCAGATACAGAGCAAGAAAGAAAGACGTC 599  
Db 556 AGAAAACAGAAAGAAACCCAGTTTTTTTTCAGATACAGAGCAAGAAAGAAAGACGTC 615  
Qy 600 TAATGGCTTTGAGTCATGAGAAATGAGAAATGAAGGAAGAGCTTGAAAACTTAAAGGGA 659  
Db 616 TAATGGCTTTGAGTCATGAGAAATGAGAAATGAAGGAAGAGCTTGAAAACTTAAAGGGA 675  
Qy 660 AATCAGAAAGGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGCCG 719  
Db 676 AATCAGAAAGGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGCCG 735  
Qy 720 AGCAGAAAAGAACCACTCAGACCCAGGTGTGAGGCTACAAGCAGAGAAAGCAGACC 779  
Db 736 AGCAGAAAAGAACCACTCAGACCCAGGTGTGAGGCTACAAGCAGAGAAAGCAGACC 795  
Qy 780 TGTGCGCATCGTGTCTGAATCTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATT 839  
Db 796 TGTGCGCATCGTGTCTGAATCTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATT 855  
Qy 840 CCTTTGTTGAAATTAGGATGGCTGAAGGAGAGCAGAGGGTCACTGAAAGAAATCAAGC 899  
Db 856 CCTTTGTTGAAATTAGGATGGCTGAAGGAGAGCAGAGGGTCACTGAAAGAAATCAAGC 915  
Qy 900 ATAGTCTCGGGCCCAAGAACAGTCTCCACTGGCAGCGCATTTGCTAAATATAGAGCA 959  
Db 916 ATAGTCTCGGGTCCACAGAAACAGTCTCCACTGGCAGCGCATTTGCTACTATAGAGGA 975  
Qy 960 GATCTCAGATGGGCGCAAGAAATTACTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCC 1019  
Db 976 GATCTCAGATGGGCGCAAGAAATTACTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCC 1035  
Qy 1020 TCGTGTGCTTAGGGAAGGGAATCAGAAAGTGAGAGACTTGAAGTTCGACTCAAGGAG 1079  
Db 1036 TCGTGTGCTTAGGGAAGGGAATCAGAAAGTGAGAGACTTGAAGTTCGACTCAAGGAG 1095  
Qy 1080 CCAAGAAAAGAGTTTCAGATTTTGAAGAAAACAAAGTAATCGTCTTCGAGATTGAACCC 1139  
Db 1096 CCAAGAAAAGAGTTTCAGATTTTGAAGAAAACAAAGTAATCGTCTTCGAGATTGAACCC 1155  
Qy 1140 AGACAGAGGGAGCAGAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTTGGAA 1199  
Db 1156 AGACAGAGGGAGCAGAGAAAGAGAAATGATGAAGAAAGGCCCGGAGACTGTTGGAA 1215

## RESULT 3

US-10-342-887-128  
; Sequence 128, Application US/10342887  
; Publication No. US20040058340A1  
; GENERAL INFORMATION:  
; APPLICANT: Dai, Hongyue  
; APPLICANT: He, Yudong  
; APPLICANT: Linsley, Peter S.  
; APPLICANT: Mao, Mao  
; APPLICANT: Roberts, Christopher J.  
; APPLICANT: Van 't Veer, Laura Johanna

Qy 1200 GCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAGAGCTTCAAGAGGCTC 1259  
Db 1216 GCGAAGTGGAGCACTGAACCTCCAGGTGACATCTCTGTTTAAGAGCTTCAAGAGGCTC 1275  
Qy 1260 ATACAAAACTCAGCGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAAGTGTCAAGCCC 1319  
Db 1276 ATACAAAACTCAGCGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAAGTGTCAAGCCC 1335  
Qy 1320 TTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTTTATA 1379  
Db 1336 TTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTTGTTTATC 1395  
Qy 1380 CTAAACAAAAAGTTAGAGCTTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAACAGG 1439  
Db 1396 CTAAACAAAAAGTTAGAGCTTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAACAGG 1455  
Qy 1440 CTAAACAAAAAGTTAGAGCTTCAAATTAATCTGTCTCAGATGACACACAAAGCTTC 1499  
Db 1456 CTAAACAAAAAGTTAGAGCTTCAAATTAATCTGTCTCAGATGACACACAAAGCTTC 1515  
Qy 1500 TTCAAGAACATTAATGCAATTTGAAACAAATTTGAGGAACTAAACAAAGAAAGAGTCAAGAA 1559  
Db 1516 TTCAAGAACATTAATGCAATTTGAAACAAATTTGAGGAACTAAACAAAGAAAGAGTCAAGAA 1575  
Qy 1560 AAGTGGACAGGGCAGTGTGTAAGGAACTGAGTGAAGAACTGGCACTGGCAGAGAAAGCTC 1619  
Db 1576 AAGTGGACAGGGCAGTGTGTAAGGAACTGAGTGAAGAACTGGCACTGGCAGAGAAAGCTC 1635  
Qy 1620 TGGCTTCCAAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATTTGCAAGAGGAAAGAGG 1679  
Db 1636 TGGCTTCCAAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATTTGCAAGAGGAAAGAGG 1695  
Qy 1680 ACTCGGAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1739  
Db 1696 ACTCGGAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1755  
Qy 1740 CTGAAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGCAAACTGGCACTTCAGCTGG 1799  
Db 1756 CTGAAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGCAAACTGGCACTTCAGCTGG 1815  
Qy 1800 CAGTTCTGCTGAAAGAGAAATGATGCTTTGCAAGACGAGGCGAGGAGTCTTGATGGAGA 1859  
Db 1816 CAGTTCTGCTGAAAGAGAAATGATGCTTTGCAAGACGAGGCGAGGAGTCTTGATGGAGA 1875  
Qy 1860 TGCAGAGTCTCATGGGCGAGAACAAAGTACTCTGACACAGAGGCTTACCTTTGTTCAA 1919  
Db 1876 TGCAGAGTCTCATGGGCGAGAACAAAGTACTCTGACACAGAGGCTTACCTTTGTTCAA 1935  
Qy 1920 GAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCCCA 1979  
Db 1936 GAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCCCA 1995  
Qy 1980 AGTGTGAGAGGTTCTGCTGACATAGACACGTTACAGATTACGTTGATGGATTCATCA 2039  
Db 1996 AGTGTGAGAGGTTCTGCTGACATAGACACGTTACAGATTACGTTGATGGATTCATCA 2055  
Qy 2040 TTTAAGTGTGATGATATCACCTCCCAAACTGTTGGT 2077  
Db 2056 TTTAAGTGTGATGATATCACCTCCCAAACTGTTGGT 2093

; APPLICANT: Van de Vijver, Marc J.  
; APPLICANT: Bernards, Rene  
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients  
; FILE REFERENCE: 9301-188-999  
; CURRENT APPLICATION NUMBER: US/10/342,887  
; CURRENT FILING DATE: 2003-01-15  
; PRIOR APPLICATION NUMBER: 60/298,918  
; PRIOR FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 60/380,710  
; PRIOR FILING DATE: 2002-05-14  
; PRIOR APPLICATION NUMBER: 10/172,118  
; PRIOR FILING DATE: 2002-06-14  
; NUMBER OF SEQ ID NOS: 2699  
; SEQ ID NO 128  
; LENGTH: 2139  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-342-887-128

Query Match 99.0%; Score 2056.4; DB 8; Length 2139;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 2071; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 1 ATCCCGTGGGAGTTCTCTCCAGCGGCGACGATGCCAGGAAACAGTGACCTGAGCGA 60  
DB |||||  
QY 61 AGCCAAAGCCGGCGGAGGTGGCTTTGATAGCTGGTGTGCCACTTCTCGGCTTGGG 120  
DB |||||  
QY 76 AGCCAAAGCCGGCGGAGGTGGCTTTGATAGCTGGTGTGCCACTTCTCGGCTTGGG 135  
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QY 121 TGAGCGGTACGCTCTGTAAACCCAACTTCTTCACTTGAACAGCTGCTGGTTCAGC 180  
DB |||||  
QY 136 TGAGCGGTACGCTCTGTAAACCCAACTTCTTCACTTGAACAGCTGCTGGTTCAGC 195  
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QY 181 ATTAATGAAGATTAGTCAGTCAGGCTGGTGTGCTGAGTCGCGACATAGAGAATCAA 240  
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QY 196 ATTAATGAAGATTAGTCAGTCAGGCTGGTGTGCTGAGTCGCGACATAGAGAATCAA 255  
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QY 241 AATGTGCCAAATGTAATCGAGAGAAAGTGGCAACTTTT - GGAGTGACTTTTCCACAG 299  
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QY 256 AATGTGCCAAATGTAATCGAGAGAAAGTGGCAACTTTTGGGAGTGACTTTTCCACAG 315  
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QY 300 GAATTTCTGCAATGTCCCACTCAACCTCTCAGCTGCTCTCACTGAAAAGGAGGACAGCCCCA 359  
DB |||||  
QY 316 GAATTTCTGCAATGTCCCACTCAACCTCTCAGCTGCTCTCACTGAAAAGGAGGACAGCCCCA 375  
DB |||||  
QY 360 GTGAAAGCACAGAAATGGAACCCCACTGCGCCCAACCAACCTGGGACACGTTTACCC 419  
DB |||||  
QY 376 GTGAAAGCACAGAAATGGAACCCCACTGCGCCCAACCAACCTGGGACACGTTTACCC 435  
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QY 420 CGGAGGAGCTGCTGACGAGATCAAGAGCTCTGACCAAGAACCCAGCTGAAAGNAG 479  
DB |||||  
QY 436 CGGAGGAGCTGCTGACGAGATCAAGAGCTCTGACCAAGAACCCAGCTGAAAGNAG 495  
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QY 480 CCATGAAGCTAAATAATCAAGCCATCAAGAGGAGATTTGAGGAGCTTTGGGCTGGACAG 539  
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QY 496 CCATGAAGCTAAATAATCAAGCCATCAAGAGGAGATTTGAGGAGCTTTGGGCTGGACAG 555  
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QY 540 AGAAAACAGAGGAGAAACCGCAGTTTTTTTGGAGATACAGAGCAAGAGCAAAAGAGCGTC 599  
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QY 616 TAATGCGCTTGAGTCATGAGAAATGAGAAATGAGAGAGAGCTTGGAAACTTAAAGGGA 675  
DB |||||  
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QY 676 AATCAGAAAGGTCATCTGAGGACCCCACTGATCACTCCAGGCTTCCAGGGCCGAGGCGG 735  
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QY 720 AGCAGGAAAGGACCAAGCTCAGGACCCAGGTCGTGAGGCTTACAGCAGAGAAAGGACGACC 779  
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DB 736 AGCAGGAAAGGACCCAGCTCAGAACCCAGGTGTGTAGGCTTACAGCAGAGAGGACGACCC 795  
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DB 780 TGTGTGGCATCGTGTCTGAACTCAGCTCAAGCTCAAGCTCAGCGGCTCTCTCAGAAAGATT 839  
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DB 796 TGTGTGGCATCGTGTCTGAACTCAGCTCAAGCTCAAGCTCAGCGGCTCTCTCAGAAAGATT 855  
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DB 840 CCTTTGTTGAAATTAGGATGGCTGAAGGAGAGCAGAGAGGTGATGTAAGAAATCAAGC 899  
QY |||||  
DB 856 CCTTTGTTGAAATTAGGATGGCTGAAGGAGAGCAGAGAGGTGATGTAAGAAATCAAGC 915  
QY |||||  
DB 900 ATAGTCTCTGGGCCACGAGAAACAGTCTCCACTGCGCAGGCACTTGTCTAAATATATAGGAGCA 959  
QY |||||  
DB 916 ATAGTCTCTGGTCCACGAGAAACAGTCTCCACTGCGCAGGCACTTGTCTCATATAGGAGGA 975  
QY |||||  
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DB 976 GATCTGCAGATGGGGCCAAAGAAATTACTTTCGAAACATGAGGAGTTAACTGTGAGCCAGCTCC 1035  
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DB 1036 TGTGTGCTTAAGGGAAGGGAATCAGAAAGGTGAGAGACTTGAAGTTGCACTCAAGGAGG 1095  
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DB 1080 CCAAGAGAAAGATTTCAGATTTTGAAGAGAAACAAAGTAATCGTCTGAGATTGAAACCC 1139  
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DB 1096 CCAAGAGAAAGATTTCAGATTTTGAAGAGAAACAAAGTAATCGTCTGAGATTGAAACCC 1155  
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DB 1140 AGACAGAGGGGACACAGAGAAAGAGAAATGATCAAGAGAAAGGCCCGGAGACTTGTTCGAA 1199  
DB |||||  
DB 1156 AGACAGAGGGGACACAGAGAAAGAGAAATGATGAGAGAAAGGCCCGGAGACTTGTTCGAA 1215  
QY |||||  
DB 1200 GCGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTC 1259  
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DB 1216 GCGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGGCTC 1275  
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DB 1260 ATACAAACCTCAGCGAGAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTGAGGCTC 1319  
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DB 1276 ATACAAACCTCAGCGAGAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTGAGGCTC 1335  
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DB 1320 TTGAAAGGAAATTTCTGCAATTCAGAGTTGAAATGAAAGAGAGAGCTTGTGTTTATA 1379  
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DB 1336 TTGAAAGGAAATTTCTGCAATTCAGAGTTGAAATGAAAGAGAGAGCTTGTGTTTATC 1395  
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DB 1380 CTAAACAAAAGTTAGAGCTTCAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAACAGG 1439  
QY |||||  
DB 1396 CTAAACAAAAGTTAGAGCTTCAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAACAGG 1455  
QY |||||  
DB 1440 CTAAACACAGAGGATGAAAGTCCAAATTTAATCTGTGTACAGATGACACAAAGGCTC 1499  
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QY |||||  
DB 1500 TTCAAGAACATATAATGCAATTTGAAACCAATTCAGGAACTTAAACAGAAAGAGGTGAGAAA 1559  
QY |||||  
DB 1516 TTCAAGAACATATAATGCAATTTGAAACCAATTCAGGAACTTAAACAGAAAGAGGTGAGAAA 1575  
QY |||||  
DB 1560 AAGTGCACAGGGCAGTGTCTCAAGGAACTGAGTGAAGAACTTGGAACTGGCAGAGAAAGGCTC 1619  
QY |||||  
DB 1576 AAGTGCACAGGGCAGTGTCTGAGGAACTGAGTGAAGAACTGAGTGAAGAAAGGCTC 1635  
QY |||||  
DB 1620 TGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATTCGCAAGCAGGAGAGG 1679  
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DB 1636 TGGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCAATTCGCAAGCAGGAGAGG 1695  
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DB 1680 ACCTGGAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1739  
QY |||||  
DB 1696 ACCTGGAACCATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1755  
QY |||||  
DB 1740 CTGAAAGAGCAGCGAGAGAGAAATTCATGAGGAAAGGAGGAGCACTGGCAATTCAGCTGG 1799  
QY |||||  
DB 1756 CTGAAAGAGCAGCGAGAGAGAAATTCATGAGGAAAGGAGGAGCACTGGCAATTCAGCTGG 1815  
QY |||||  
DB 1800 CAGTCTCTGTAAGAGAAATGATGCTTTCGAAACGCGAGGAGGAGCTCTCTGATGAGGA 1859  
QY |||||  
DB 1816 CAGTCTCTGTAAGAGAAATGATGCTTTCGAAACGCGAGGAGGAGCTCTCTGATGAGGA 1875  
QY |||||





Qy	1440	CTAATAACAGACGAGTGAAGTCCAAATTAACTGTGCTTACAGATGACACACAAAGCTTC	1499
Db	1456	CTAATAACAGACGAGTGAAGTCCAAATTAACTGTGCTTACAGATGACACACAAAGCTTC	1515
Qy	1500	TTCAAGAACATAAATAATGCATTGAAACAAATTGAGGAACATAACAAGAAAAAGAGTCAGAAA	1559
Db	1516	TTCAAGAACATAAATAATGCATTGAAACAAATTGAGGAACATAACAAGAAAAAGAGTCAGAAA	1575
Qy	1560	AAGTGGACAGGGCAGTGCCTGAAGGAACTGAGTGTAAAAAATGTGGAACTGGCAGAGAAGCTC	1619
Db	1576	AAGTGGACAGGGCAGTGCCTGAAGGAACTGAGTGTAAAAAATGTGGAACTGGCAGAGAAGCTC	1635
Qy	1620	TGGCTTCCAAACAGCTGCACAAATGATGAAATGAAGACAAACCATGTGCCAAGCAGGAAGAGG	1679
Db	1636	TGGCTTCCAAACAGCTGCACAAATGATGAAATGAAGACAAACCATGTGCCAAGCAGGAAGAGG	1695
Qy	1680	ACCTGGAAACCATGACCACTCTCAGGGCTCAGATGGAAAGTTACTGTTTCTGATTTTCATG	1739
Db	1696	ACCTGGAAACCATGACCACTCTCAGGGCTCAGATGGAAAGTTACTGTTTCTGATTTTCATG	1755
Qy	1740	CTGAAGACGACGAGGAGAGGAAATTCATGAGGAAAAAGGACCACTGGCATTGCAAGCTGG	1799
Db	1756	CTGAAGACGACGAGGAGAGGAAATTCATGAGGAAAAAGGACCACTGGCATTGCAAGCTGG	1815
Qy	1800	CAGTTCTGCTGAAAGAGAAATGATGCTTTCGAAGACGGAGGCAGGCAGTCTCTTGATGAGA	1859
Db	1816	CAGTTCTGCTGAAAGAGAAATGATGCTTTCGAAGACGGAGGCAGGCAGTCTCTTGATGAGA	1875
Qy	1860	TGCAGAGTCGTATGGGCGAGAAACAAGTGACTCTGACCAAGAGCTTACCTTGTTCAAA	1919
Db	1876	TGCAGAGTCGTATGGGCGAGAAACAAGTGACTCTGACCAAGAGCTTACCTTGTTCAAA	1935
Qy	1920	GAGAGCTGTAGGACAGGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCGCCCA	1979
Db	1936	GAGAGCTGTAGGACAGGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCGCCCA	1995
Qy	1980	AGTGTGGAGAGGTTCTGCCTGACATAGACAGCTTTACAGATTCACGTGATGGATTGCATCA	2039
Db	1996	AGTGTGGAGAGGTTCTGCCTGACATAGACAGCTTTACAGATTCACGTGATGGATTGCATCA	2055
Qy	2040	TTTAAAGTTTGATGTATCACTCTCCCAAAACTGTTGGT	2077
Db	2056	TTTAAAGTTTGATGTATCACTCTCCCAAAACTGTTGGT	2093

## RESULT 5

```

US-10-756-149-2698
; Sequence 2698, Application US/10756149
; Publication No. US20050181375A1
; GENERAL INFORMATION:
; APPLICANT: Aziz, Natasha
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: NOVEL METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER, COMPOSITIONS AND
; TITLE OF INVENTION: METHODS OF SCREENING FOR MODULATORS OF METASTATIC CANCER
; FILE REFERENCE: file
; CURRENT APPLICATION NUMBER: US/10/756,149
; CURRENT FILING DATE: 2004-01-12
; NUMBER OF SEQ ID NOS: 5818
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2698
; LENGTH: 2139
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-10-756-149-2698

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Query March 99.0%; Score 2056.4; DB 10; Length 2139;  
 Best Local Similarity 99.7%; Pred. No. 0;  
 Matches 2071; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

Qy 1 ATCCCGTTCGGAGTTCTCTCAGGCGGCGACGATGCCGAGGAAACAGTGCACCTGTAGCGA 60  
 Db 16 ATCCCGTTCGGAGTTCTCTCAGGCGGCGACGATGCCGAGGAAACAGTGCACCTGTAGCGA 75

Qy	61	AGCCAA	GC	CGGG	CGGC	GAGTGTGCTTTGATAGTGTGTGTCACATTTCTGGCCTTTGGA	120		
Db	76	AGCCAA	GC	CGGG	CGGC	GAGTGTGCTTTGATAGTGTGTGTGTCACATTTCTGGCCTTTGGA	135		
Qy	121	TGAGCC	GT	CAGC	CTCTGTAACCCACCTTCTCACCTTTGAAACAGCTGCTGGTTCAGC	180			
Db	136	TGAGCC	GT	CAGC	CTCTGTAACCCACCTTCTCACCTTTGAAACAGCTGCTGGTTCAGC	195			
Qy	181	ATTAAT	GAAGA	TTAGTC	CAGTGACAGGCGCTGGTGTGCTGAGTCCGCAATAGAAAGAAATCAA	240			
Db	196	ATTAAT	GAAGA	TTAGTC	CAGTGACAGGCGCTGGTGTGCTGAGTCCGCAATAGAAAGAAATCAA	255			
Qy	241	AAATGT	CCAAA	TGTA	CTGGAGAGAAAGTGGGCAACTTTT - GGAGTGACTTTTTCACAG	299			
Db	256	AAATGT	CCAAA	TGTA	CTGGAGAGAAAGTGGGCAACTTTTGGGAGTGACTTTTTCACAG	315			
Qy	300	GAAC	TTCTGCA	ATGTGCC	CATCAACCTCTCAGCTGTCCTCACTGAAAAGGAGGACAGCCCCA	359			
Db	316	GAAC	TTCTGCA	ATGTGCC	CATCAACCTCTCAGCTGTCCTCACTGAAAAGGAGGACAGCCCCA	375			
Qy	360	GTGAAA	GC	CAGGAA	ATGGAACCCCCACCTTGGGCCCAACCCAAACCTTGACACAGTTTACCC	419			
Db	376	GTGAAA	GC	CAGGAA	ATGGAACCCCCACCTTGGGCCCAACCCAAACCTTGACACAGTTTACCC	435			
Qy	420	CGGAGG	AGCTGCTGC	CAGCAGATGA	AGAGCTCTCTGACCAAGAACCCACCGCTGAAAGAAG	479			
Db	436	CGGAGG	AGCTGCTGC	CAGCAGATGA	AGAGCTCTCTGACCGGAGAACCCACCGCTGAAAGAAG	495			
Qy	480	CCATGA	AGCTTA	ATAATCA	AGCCATGAAGGGAGATTTGAGGAGCTTCCGGCCTGGACAG	539			
Db	496	CCATGA	AGCTTA	ATAATCA	AGCCATGAAGGGAGATTTGAGGAGCTTCCGGCCTGGACAG	555			
Qy	540	AGAA	CA	GAGA	AGGAAGACGCCAGTTTTCAGATACAGACCAAGAAAGCAAAAGAGCGTC	599			
Db	556	AGAA	CA	GAGA	AGGAAGACGCCAGTTTTCAGATACAGACCAAGAAAGCAAAAGAGCGTC	615			
Qy	600	TAAT	TGGC	TTGAGT	CATGAGAAATGAGAAATGGAAGGAAGAGCTTGGAAAACTAAAAAGGA	659			
Db	616	TAAT	TGGC	TTGAGT	CATGAGAAATGAGAAATGGAAGGAAGAGCTTGGAAAACTAAAAAGGA	675			
Qy	660	AATC	AGAA	AGGT	CATCTGAGAGCCCACTGATGACTCCAGGCTTCCAGAGGCCGGAAGCGG	719			
Db	676	AATC	AGAA	AGGT	CATCTGAGAGCCCACTGATGACTCCAGGCTTCCAGAGGCCGGAAGCGG	735			
Qy	720	AGCAGG	AAAA	AGGAC	CAGCTCAGGACCCAGGTGTGTAGGCTTACAAGCAGAGAAAGCAGACC	779			
Db	736	AGCAGG	AAAA	AGGAC	CAGCTCAGGACCCAGGTGTGTAGGCTTACAAGCAGAGAAAGCAGACC	795			
Qy	780	TGTT	TGGC	ATCGTGT	GTGAACCTCAGCTCAAGCTGAACCTCCAGCGGCTCCTCAGAAAGATT	839			
Db	796	TGTT	TGGC	ATCGTGT	GTGAACCTCAGCTCAAGCTGAACCTCCAGCGGCTCCTCAGAAAGATT	855			
Qy	840	CC	TTTGT	TGAA	ATTAGGATGGCTGAAGGAGAACGAGAGGGTCACTAAAAGAAATCAAGC	899			
Db	856	CC	TTTGT	TGAA	ATTAGGATGGCTGAAGGAGAACGAGAGGGTCACTAAAAGAAATCAAGC	915			
Qy	900	ATAG	TC	CTGG	CCACGAGAAACAGTCTCCACTGCGCAGCATTTGTCTAAATATAGGAGCA	959			
Db	916	ATAG	TC	CTGG	CCACGAGAAACAGTCTCCACTGCGCAGCATTTGTCTAAATATAGGAGCA	975			
Qy	960	GAT	CTG	CAGATGGG	CCAGAATTA	CTTCGAACATGAGGATTTAACTGTGAGCGCAGCTCC	1019		
Db	976	GAT	CTG	CAGATGGG	CCAGAATTA	CTTCGAACATGAGGATTTAACTGTGAGCGCAGCTCC	1035		
Qy	1020	TG	CTGTG	CC	TAAAGGGAAGGGAATCAGAGGTGAGAGACTTGAAGTTGC	ACTCAAGGAGG	1079		
Db	1036	TG	CTGTG	CC	TAAAGGGAAGGGAATCAGAGGTGAGAGACTTGAAGTTGC	ACTCAAGGAGG	1095		
Qy	1080	CCAA	GA	AGAA	CAGTTT	CAGATTTTGA	AAAGAAAACAAGTAATCGTTCTGAGATTTGA	AACCC	1139
Db	1096	CCAA	GA	AGAA	CAGTTT	CAGATTTTGA	AAAGAAAACAAGTAATCGTTCTGAGATTTGA	AACCC	1155
Qy	1140	AG	CA	GAGG	GGG	AGCA	CAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTTGTGGAA	1199	

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Db 1156 ACACAGAGGGAGCAGACAGAGAAAGAGATGATGAAGAGAAAGCGCCGGAGACTGTTGGAA 1215
QY 1200 GCGAAGTGAAGACACTGAACCTCCAGGTGCATCTCTGTTTAAAGAGCTTCAAGAGGCTC 1259
Db 1216 GCGAAGTGAAGACACTGAACCTCCAGGTGCATCTCTGTTTAAAGAGCTTCAAGAGGCTC 1275
QY 1260 ATACAAAACCTCAGCAGAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAGTCTCAGGGCC 1319
Db 1276 ATACAAAACCTCAGCAGAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAGTCTCAGGGCC 1335
QY 1320 TTGAAGGAAAAATTTCTGCAATTTCCATCAGAGTTGAATGAAAAGCAAGAGCTTGTATTATA 1379
Db 1336 TTGAAGGAAAAATTTCTGCAATTTCCATCAGAGTTGAATGAAAAGCAAGAGCTTGTATTATC 1395
QY 1380 CTAAACAAAAGTTAGAGCTACAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGG 1439
Db 1396 CTAAACAAAAGTTAGAGCTACAGTGGAAAGCATGCTATCAGAAATCAAAATGGAACAGG 1455
QY 1440 CTAAACACAGGATGAAAAGTCCAAATTAACCTGTCTACAGATGACACACAACAGCTTC 1499
Db 1456 CTAAACACAGGATGAAAAGTCCAAATTAACCTGTCTACAGATGACACACAACAGCTTC 1515
QY 1500 TTCAAGAACATAATATGCAATTTGAAAAACAATTCAGGAACCTAACAGAAAAGAGTCAGAAA 1559
Db 1516 TTCAAGAACATAATATGCAATTTGAAAAACAATTCAGGAACCTAACAGAAAAGAGTCAGAAA 1575
QY 1560 AAGTGCAGAGGAGTGTGAGGAACCTGAGTGAAGAACTGAGTGAAGAACTGGCAGAGAGGCTC 1619
Db 1576 AAGTGCAGAGGAGTGTGAGGAACCTGAGTGAAGAACTGAGTGAAGAACTGGCAGAGAGGCTC 1635
QY 1620 TGCGTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCATTCGCAAGCAGGAAGAGG 1679
Db 1636 TGCGTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCATTCGCAAGCAGGAAGAGG 1695
QY 1680 ACCTGGAACCCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1739
Db 1696 ACCTGGAACCCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTCATG 1755
QY 1740 CTGAAGACAGCGAGAGAGAAAATTCATGAGGAAAAGAGCAACTGGCATTCGCAGCTGG 1799
Db 1756 CTGAAGACAGCGAGAGAGAAAATTCATGAGGAAAAGAGCAACTGGCATTCGCAGCTGG 1815
QY 1800 CAGTTCTGCTGAAAGAGATGATGCTTTTCAAGACGAGGAGGAGCACTCTTGTATGGAGA 1859
Db 1816 CAGTTCTGCTGAAAGAGATGATGCTTTTCAAGACGAGGAGGAGCACTCTTGTATGGAGA 1875
QY 1860 TGCAGAGTCTCATGGGGCGAGAACAAAGTGACTCTGACACAGAGGCTTACCTTGTTCAAA 1919
Db 1876 TGCAGAGTCTCATGGGGCGAGAACAAAGTGACTCTGACACAGAGGCTTACCTTGTTCAAA 1935
QY 1920 GAGGAGCTGAGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCAATTCCTGCCCCA 1979
Db 1936 GAGGAGCTGAGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCAATTCCTGCCCCA 1995
QY 1980 AGTGTGAGAGGTTCTGCTGACATAGACAGCTTACAGATTACAGTATGGATTGATCA 2039
Db 1996 AGTGTGAGAGGTTCTGCTGACATAGACAGCTTACAGATTACAGTATGGATTGATCA 2055
QY 2040 TTTAAGTGTGTATGATACCTCCCAAACTGTTGGT 2077
Db 2056 TTTAAGTGTGTATGATACCTCCCAAACTGTTGGT 2093
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## RESULT 6

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US-10-609-133-5
; Sequence 5, Application US/10609133
; Publication No. US20040191798A1
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut Health Center
; APPLICANT: Sarfarazi, Mansoor
; APPLICANT: Rezaie, Tayebbeh
; APPLICANT: Child, Anne H
```

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; TITLE OF INVENTION: Optineurin and Glaucoma
; FILE REFERENCE: UCT-0046P2
; CURRENT APPLICATION NUMBER: US/10/609,133
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10,281,457
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 10,090,118
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 10,060,981
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/344,754
; PRIOR FILING DATE: 2001-12-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 2008
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; AUTHORS: Rezaie et al.
; TITLE: Adult-Onset Primary Open-Angle Glaucoma Caused by Mutations in
; TITLE: Optineurin
; JOURNAL: Science
; VOLUME: 295
; ISSUE: 5557
; PAGES: 1077-1079
; DATE: 2002
; DATABASE ACCESSION NUMBER: AF420373
; DATABASE ENTRY DATE: 2002-02-11
; RELEVANT RESIDUES: (1)..(2008)
US-10-609-133-5

Query Match 92.8%; Score 1927.4; DB 9; Length 2008;
Best Local Similarity 96.6%; Pred. No. 0; Mismatches 1; Indels 69; Gaps 1;
Matches 2007; Conservative 0;

QY 1 ATCCCGGTGGGAGTTCTCTCCAGCGCGCAGCATCCGAGGAAACAGTGACCCCTGAGCGA 60
Db 1 ATCCCGGTGGGAGTTCTCTCCAGCGCGCAGCATCCGAGGAAACAGTGACCCCTGAGCGA 60
QY 61 AGCCAAAGCGGGCGGCGAGGTGGCTTTGATAGCTGGTGGTCCCACTTCCTGGCCTTGA 120
Db 61 AGCCAAAGCGGGCGGCGAGGTGGCTTTGATAGCTGGTGGTCCCACTTCCTGGCCTTGA 120
QY 121 TGAGCCGTACGCTCTGTAAACCCCAACTTCCTCACCTTTGAAACAGCTGCTGTTTCAGC 180
Db 121 TGAGCCGTACGCTCTGTAAACCCCAACTTCCTCACCTTTGAAACAGCTGCTGTTTCAGC 180
QY 181 ATTAATGAAGATTAGTCAAGTGAAGCCCTGGTGTGCTGAGTCCGACATAGAAGATCAA 240
Db 181 ATTAATGAAGATTAGTCAAGTGAAGCCCTGGTGTGCTGAGTCCGACATAGAAGATCAA 240
QY 241 AAATGTCCAAATGTAATCTGGAGAGAAAGTGGGCAACTTTTGGAGTGACTTTTCCACAGG 300
Db 231 -----G 231
QY 301 RACTTCTCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGAGGACAGCCCCAG 360
Db 232 RAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAAGGAGGACAGCCCCAG 291
QY 361 TGAAGACACAGGAAATGGAACCCCACTGGCCCAACCCAAACCTTGGACACGCTTTACCCC 420
Db 292 TGAAGACACAGGAAATGGAACCCCACTGGCCCAACCCAAACCTTGGACACGCTTTACCCC 351
QY 421 GGAGAGCTGCTGCAGCAGATGAAAGAGCTCTCTGACCAAGAACCCACAGCTGAAGAAGC 480
Db 352 GGAGAGCTGCTGCAGCAGATGAAAGAGCTCTCTGACCCGAGAACCCACAGCTGAAGAAGC 411
QY 481 CATGAAGCTAAATAATCAAGCCATCAAGGGGAGATTGAGGAGCTTTCCGCTTGGACAGA 540
Db 412 CATGAAGCTAAATAATCAAGCCATCAAGGGGAGATTGAGGAGCTTTCCGCTTGGACAGA 471
QY 541 GAAACAGAGGAAGAACGCCAGTTTGTGAGATACAGCAAGAACAGAAAGAGCGCTCT 600
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Query Match		85.7%;	Score 1779.4;	DB 8;	Length 2327;	
Best Local Similarity		99.9%;	Pred. No. 0;			
Matches 1780;		Conservative	0;	Mismatches	1;	Indels 0; Gaps 0;
Qy	297	CAGGAACCTTCTGCATATCCCATCAACCTCTCAGCTGCCTCAGTGAAGAGGACGACGCC	356			
Db	141	CAGGAACCTTCTGCATATCCCATCAACCTCTCAGCTGCCTCAGTGAAGAGGACGACGCC	200			
Qy	357	CCAGTGAAGCACAGGAAATGGACCCGCCACCTGGGCCACCCAAACCTCGACACGTTTA	416			
Db	201	CCAGTGAAGCACAGGAAATGGACCCGCCACCTGGGCCACCCAAACCTCGACACGTTTA	260			
Qy	417	CCCCGAGGAGCTGCTCAGCAGATGAAGAGCTCTTGACCAAGAACCCACAGCTGAAG	476			
Db	261	CCCCGAGGAGCTGCTCAGCAGATGAAGAGCTCTTGACCGAGAACCCACAGCTGAAG	320			
Qy	477	AAGCCATGAAGCTTAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCTTGA	536			
Db	321	AAGCCATGAAGCTTAATAATCAAGCCATGAAGGGAGATTGAGGAGCTTTCGGCTTGA	380			
Qy	537	CAGAGAAACAGAGGAAGACGCCAGTCTTTTTCAGATACAGAGCAAGAGAGCAAGAGC	596			
Db	381	CAGAGAAACAGAGGAAGACGCCAGTCTTTTTCAGATACAGAGCAAGAGAGCAAGAGC	440			
Qy	597	GTCTAATGGCTTGAATCATGAGATGAGAAATTTGAAGGAAGAGCTTTGGAAGAACTAAAG	656			
Db	441	GTCTAATGGCTTGAATCATGAGATGAGAAATTTGAAGGAAGAGCTTTGGAAGAACTAAAG	500			
Qy	657	GGAAATCAGAAAGTCTATCTGAGACCCCACTGATGATCTCAGGCTTCCAGGGCCGAAG	716			
Db	501	GGAAATCAGAAAGTCTATCTGAGACCCCACTGATGATCTCAGGCTTCCAGGGCCGAAG	560			
Qy	717	CGAGCAGGAAAGGACAGCTCAGGACCCAGAGTGTGAGGCTACAGCAGAGAGAGCAG	776			
Db	561	CGAGCAGGAAAGGACAGCTCAGGACCCAGAGTGTGAGGCTACAGCAGAGAGAGCAG	620			
Qy	777	ACCTGTGTGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG	836			
Db	621	ACCTGTGTGGCATCGTGTCTGAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAG	680			
Qy	837	ATTCTTTTGTGAAATTTAGATGGCTGAAGAGAGACAGAGAGGTGATGTAAGAAATCA	896			
Db	681	ATTCTTTTGTGAAATTTAGATGGCTGAAGAGAGACAGAGAGGTGATGTAAGAAATCA	740			
Qy	897	ASCATAGTCTGGGCCCCACAGAACAGTCTCCACTGGCAGCGATTCTCTAAATATAGGA	956			
Db	741	ASCATAGTCTGGGCCCCACAGAACAGTCTCCACTGGCAGCGATTCTCTAAATATAGGA	800			
Qy	957	GCAGATCTGCAGATGGGCCCAAGAAATTAATTCGAAATAGAGAGTTAACTGTGAGCCAGC	1016			
Db	801	GCAGATCTGCAGATGGGCCCAAGAAATTAATTCGAAATAGAGAGTTAACTGTGAGCCAGC	860			
Qy	1017	TCCTGTCTGCCCTAAGGGAAAGGAAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGG	1076			
Db	861	TCCTGTCTGCCCTAAGGGAAAGGAAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGG	920			
Qy	1077	AGGCCAAGAAAGAGTTTCAGATTTTGAAAGAAACAACTAATCGTTCTGAGATTGAAA	1136			
Db	921	AGGCCAAGAAAGAGTTTCAGATTTTGAAAGAAACAACTAATCGTTCTGAGATTGAAA	980			
Qy	1137	CCCAGACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCGGAGACTGTTG	1196			
Db	981	CCCAGACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAGAAAGGCCCGGAGACTGTTG	1040			
Qy	1197	GAGCGAAGTGGAGCACTGAACCTCCAGTGACATCTCTGTTTAAGGAGCTTCAAGAGG	1256			
Db	1041	GAGCGAAGTGGAGCACTGAACCTCCAGTGACATCTCTGTTTAAGGAGCTTCAAGAGG	1100			
Qy	1257	CTCATACAAACTCAGCGAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTGAGG	1316			
Db	1101	CTCATACAAACTCAGCGAAGCTGAGCTAATGAGAGAGACTTCAAGAAAGTGTGAGG	1160			

Qy	1317	CCCTTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAAAGCAAGAGCTTGTTC	1376
Db	1161	CCCTTGAAAGGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAAAGCAAGAGCTTGTTC	1220
Qy	1377	ATATCTAACAAAAAGTTAGAGCTTCAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAC	1436
Db	1221	ATATCTAACAAAAAGTTAGAGCTTCAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAC	1280
Qy	1437	AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATTGACACAAACAAGC	1496
Db	1281	AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATTGACACAAACAAGC	1340
Qy	1497	TTCTTCAAGAACATAATAATGCAATGAAACCAATTCAGGAACTTAAACAAGAAAAAGAGTCAG	1556
Db	1341	TTCTTCAAGAACATAATAATGCAATGAAACCAATTCAGGAACTTAAACAAGAAAAAGAGTCAG	1400
Qy	1557	AAAAAGTGCACAGGGCAGTGTGAAGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGG	1616
Db	1401	AAAAAGTGCACAGGGCAGTGTGAAGAACTGAGTGAAGAACTGGAACCTGGCAGAGAGG	1460
Qy	1617	CTCTGGCTTCCAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAGGAAG	1676
Db	1461	CTCTGGCTTCCAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAGGAAG	1520
Qy	1677	AGGACCTGGAACCATATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGATTTTC	1736
Db	1521	AGGACCTGGAACCATATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGATTTTC	1580
Qy	1737	ATGCTGAAAGAGCGGAGAGAGAAAAATTCATGAGAAAGGAGCAACTGGCAATTCGAGC	1796
Db	1581	ATGCTGAAAGAGCGGAGAGAGAAAAATTCATGAGAAAGGAGCAACTGGCAATTCGAGC	1640
Qy	1797	TGGCAGTCTCTGCTGAAAGAGAAATGATGCTTTCGAAGACGGAGCAGGAGTCTCTGATGG	1856
Db	1641	TGGCAGTCTCTGCTGAAAGAGAAATGATGCTTTCGAAGACGGAGCAGGAGTCTCTGATGG	1700
Qy	1857	AGATGAGAGTCTGATGGGGGAGAAACAAAGTGAATCTCTGACAGAGGCTTACCTTGTTC	1916
Db	1701	AGATGAGAGTCTGATGGGGGAGAAACAAAGTGAATCTCTGACAGAGGCTTACCTTGTTC	1760
Qy	1917	AAAGAGAGTGGAGCAGGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCC	1976
Db	1761	AAAGAGAGTGGAGCAGGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCC	1820
Qy	1977	CCAAAGTGTGGAGAGTTCTGCTGACATAGACACAGTTACAGATTACAGTGGATTGCA	2036
Db	1821	CCAAAGTGTGGAGAGTTCTGCTGACATAGACACAGTTACAGATTACAGTGGATTGCA	1880
Qy	2037	TCATTTAAGTGTGATGATATCACCTCCCAAACTGTGGT	2077
Db	1881	TCATTTAAGTGTGATGATATCACCTCCCAAACTGTGGT	1921

RESULT 9

US-10-956-157-2378  
; Sequence 2378, Application US/10956157  
; Publication No. US20050118625A1

GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2378

; LENGTH: 2327

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-956-157-2378

Query Match		85.7%;	Score 1779.4;	DB 10;	Length 2327;		
Best Local Similarity		99.9%;	Pred. No. 0;				
Matches 1780;		Conservative	0;	Mismatches	1;	Indels	0; Gaps 0;
QY	297	CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCTCTGAAAGAGGACGAGCC	356				
DB	141	CAGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCTCTGAAAGAGGACGAGCC	200				
QY	357	CCAGTGAAGACAGAGAAATGACCCGCCACCTGSCCCACCAACCTGGACAGCTTTA	416				
DB	201	CCAGTGAAGACAGAGAAATGACCCGCCACCTGSCCCACCAACCTGGACAGCTTTA	260				
QY	417	CCCCGAGAGAGCTGCTGCAGCAGATGAAGAGCTCCTGACCAAGAACCAACAGCTGAAAG	476				
DB	261	CCCCGAGAGAGCTGCTGCAGCAGATGAAGAGCTCCTGACCAAGAACCAACAGCTGAAAG	320				
QY	477	AAGCCATGAAGCTAAATAATCAAGCCATGAAGAGATTTGAGAGATTTGAGAGCTTTCCGCTGGA	536				
DB	321	AAGCCATGAAGCTAAATAATCAAGCCATGAAGAGATTTGAGAGATTTGAGAGCTTTCCGCTGGA	380				
QY	537	CAGAGAAACAGAGGAAGAACCCAGTCTTTTGAAGATACAGAGCAAGAGCAAAAGAGC	596				
DB	381	CAGAGAAACAGAGGAAGAACCCAGTCTTTTGAAGATACAGAGCAAGAGCAAAAGAGC	440				
QY	597	GTCTAATGGCCTTGAGTCAATGAGATGAGAAATTTGAAGGAAGAGCTTTGAAAACCTAAAG	656				
DB	441	GTCTAATGGCCTTGAGTCAATGAGATGAGAAATTTGAAGGAAGAGCTTTGAAAACCTAAAG	500				
QY	657	GGAATCAGAAAGGTCAATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG	716				
DB	501	GGAATCAGAAAGGTCAATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAAG	560				
QY	717	CGAGCAGGAAGAGGACCACTCAGGACCCAGCTGAGGCTACAGCAGAGAGGCGAG	776				
DB	561	CGAGCAGGAAGAGGACCACTCAGGACCCAGCTGAGGCTACAGCAGAGAGGCGAG	620				
QY	777	ACCTGTTGGGCATCGTGTCTGAACTCAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG	836				
DB	621	ACCTGTTGGGCATCGTGTCTGAACTCAGCTCAAGCTCAAGCTCAAGCTCAAGCTCAAG	680				
QY	837	ATTCTTTTGTGAAATAGATGGCTGGAAGGAGAGCAGAGGCTCAGTAAAGAAATCA	896				
DB	681	ATTCTTTTGTGAAATAGATGGCTGGAAGGAGAGCAGAGGCTCAGTAAAGAAATCA	740				
QY	897	AGCATAGTCTGGGCCACGAGAACAGTCTCCACTGGCAGCGATCTCTAATATAGGA	956				
DB	741	AGCATAGTCTGGGCCACGAGAACAGTCTCCACTGGCAGCGATCTCTAATATAGGA	800				
QY	957	GCAGATCTGCAGATGGGCCCAAGAAATTAATCTCGAAATGAGGAGTTAACTGTGAGCCAGC	1016				
DB	801	GCAGATCTGCAGATGGGCCCAAGAAATTAATCTCGAAATGAGGAGTTAACTGTGAGCCAGC	860				
QY	1017	TCTGCTGTGCTTAAGGGAAGGGAATCAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGG	1076				
DB	861	TCTGCTGTGCTTAAGGGAAGGGAATCAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGG	920				
QY	1077	AGGCCAAAGAAAGAGTTTTCAGATTTTGAAGAAACAAAGTAACTCTCTGAGATTGAAA	1136				
DB	921	AGGCCAAAGAAAGAGTTTTCAGATTTTGAAGAAACAAAGTAACTCTCTGAGATTGAAA	980				
QY	1137	CCCAGACAGAGGGGACACAGAGAAAGAGAATGATGAAGAGAAAGGCCCGGAGACTGTTG	1196				
DB	981	CCCAGACAGAGGGGACACAGAGAAAGAGAATGATGAAGAGAAAGGCCCGGAGACTGTTG	1040				
QY	1197	GAGCGAAGTGAAGACATGAACCTCAGGTGACATCTCTGTTTAAGAGAGCTTCAAGAGG	1256				
DB	1041	GAGCGAAGTGAAGACATGAACCTCAGGTGACATCTCTGTTTAAGAGAGCTTCAAGAGG	1100				
QY	1257	CTCATACAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGGTGTCAGG	1316				
DB	1101	CTCATACAAACCTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGGTGTCAGG	1160				
QY	1317	CCCTTGAAGGAAAAATCTGCAATTCATCAGATGTTGAATGAAAAAGAGAGCTTGTGTTT	1376				

DB	1161	CCCTTGAAGGAAAAATTTCTCAATTCATCAGAGTTCAATGAAAGCAAGAGCTTGTGTTT	1220				
QY	1377	ATACTAACAAAAAGTTAGAGCTACAGTGGAAAGCATCTCTACAGAAATCAAAATGGAAAC	1436				
DB	1221	ATACTAACAAAAAGTTAGAGCTACAGTGGAAAGCATCTCTACAGAAATCAAAATGGAAAC	1280				
QY	1437	AGGCTFAAAACAGAGGATGAAAGTCCAAATTAACCTGTCTACAGATGACACAAACAAGC	1496				
DB	1281	AGGCTFAAAACAGAGGATGAAAGTCCAAATTAACCTGTCTACAGATGACACAAACAAGC	1340				
QY	1497	TTCTTCAAGAACATAATATCATTTGAAAAACAATTTGAGGAACTAAACAAGAAAGAGTCAG	1556				
DB	1341	TTCTTCAAGAACATAATATCATTTGAAAAACAATTTGAGGAACTAAACAAGAAAGAGTCAG	1400				
QY	1557	AAAAAGTGGACAGGGCAGTCTGAAGGAACTGAGTGAAGAACTGAACTGGCAGAGAGG	1616				
DB	1401	AAAAAGTGGACAGGGCAGTCTGAAGGAACTGAGTGAAGAACTGAACTGGCAGAGAGG	1460				
QY	1617	CTCTGGCTTCCAAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCACTTGCAGAGGAGG	1676				
DB	1461	CTCTGGCTTCCAAAACAGCTGCAAAATGGATGAAATGAAGCAAAACCACTTGCAGAGGAGG	1520				
QY	1677	AGGACCTGGAAACCAATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC	1736				
DB	1521	AGGACCTGGAAACCAATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC	1580				
QY	1737	ATGCTGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCATTTGCAGC	1796				
DB	1581	ATGCTGAAGAGCAGCAGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCATTTGCAGC	1640				
QY	1797	TGGCAGTTCTGCTGAAAGAGAGATGATGCTTTTGAAGACGGAGGAGGAGCTCTTTGATGG	1856				
DB	1641	TGGCAGTTCTGCTGAAAGAGAGATGATGCTTTTGAAGACGGAGGAGGAGCTCTTTGATGG	1700				
QY	1857	AGATCAGAGTCTGTCATGGGCGAGAAACAAGTGACTCTGACAGCAGGCTTACCTTGTTC	1916				
DB	1701	AGATCAGAGTCTGTCATGGGCGAGAAACAAGTGACTCTGACCCAGCAGGCTTACCTTGTTC	1760				
QY	1917	AAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCTCTGCTCC	1976				
DB	1761	AAAGAGGAGCTGAGGACAGGAGCTGGCGGCAACAGCGGAATATTCGGATTCTCTGCTCC	1820				
QY	1977	CCAAAGTGGAGAGGTTCTGCTGACATAGACACCTTACAGATTCACTGATGGATTGCA	2036				
DB	1821	CCAAAGTGGAGAGGTTCTGCTGACATAGACACCTTACAGATTCACTGATGGATTGCA	1880				
QY	2037	TCATTAAAGTGTGATGATATCACTCCCAAACTGTTGGT	2077				
DB	1881	TCATTAAAGTGTGATGATATCACTCCCAAACTGTTGGT	1921				

RESULT 10

US-10-956-157-5027

; Sequence 5027, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 5027

; LENGTH: 2296

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-956-157-5027

Query Match 85.6%; Score 1777.8; DB 10; Length 2296;



Best Local Similarity 99.9%; Pred. No. 0;			
Matches 1779; Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	297	CAGGAACTTCTGCAATGCCCATCAACTCTCAGCTGCTCAGCTCACTGAAAGGAGGACAGCC	356
Db	132	CAGGAACTTCTGCAATGCTCCATCAACTCTCAGCTGCTCAGCTCACTGAAAGGAGGACAGCC	191
Qy	357	CCAGTGAAGCACAGGAAATGGACCCGCCCACTGGGCCACCCAAAACCTGGACACGTTTA	416
Db	192	CCAGTGAAGCACAGGAAATGGACCCGCCCACTGGGCCACCCAAAACCTGGACACGTTTA	251
Qy	417	CCCCGAGGAGCTCTCAGCAGATGAAGAGCTCTGACCAAGAACCCACCGCTGAAG	476
Db	252	CCCCGAGGAGCTCTCAGCAGATGAAGAGCTCTGACCGAAGCCACCGCTGAAG	311
Qy	477	AAGCCATGAAGCTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTGGCCCTGGA	536
Db	312	AAGCCATGAAGCTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTGGCCCTGGA	371
Qy	537	CAGAGAAACAGAGAAAGCGCCAGCTTTTGTGATACAGAGCAAAAGAACGAAAGAGC	596
Db	372	CAGAGAAACAGAGAAAGCGCCAGCTTTTGTGATACAGAGCAAAAGAACGAAAGAGC	431
Qy	597	GTCTAATGGCTTGAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT	656
Db	432	GTCTAATGGCTTGAAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAGT	491
Qy	657	GGAATCAGAAAGGTCTCTGAGGACCCCACTGATGATCTCAGGCTTCCAGGCGCGAAG	716
Db	492	GGAATCAGAAAGGTCTCTGAGGACCCCACTGATGATCTCAGGCTTCCAGGCGCGAAG	551
Qy	717	CGGAGCAGGAAAGGACAGCTCAGGACCCCACTGAGGCTCAAGAGAGAGGAGGAGC	776
Db	552	CGGAGCAGGAAAGGACAGCTCAGGACCCCACTGAGGCTCAAGAGAGAGGAGGAGC	611
Qy	777	ACCTGTTGGGATCGTCTGAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG	836
Db	612	ACCTGTTGGGATCGTCTGAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTG	671
Qy	837	ATTCCTTTGTTGAAATAGGATGCTCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	896
Db	672	ATTCCTTTGTTGAAATAGGATGCTCAAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG	731
Qy	897	AGCATGCTCTGGGCCCAAGAGACAGTCTCACTGCGCAGCGCATTTGTCTAAATATAGGA	956
Db	732	AGCATGCTCTGGGCCCAAGAGACAGTCTCACTGCGCAGCGCATTTGTCTAAATATAGGA	791
Qy	957	GCAGATCTGAGATGGGCGCAAGAAATTAATTCGAACATGAGGAGTTAACTGTGAGCCAGC	1016
Db	792	GCAGATCTGAGATGGGCGCAAGAAATTAATTCGAACATGAGGAGTTAACTGTGAGCCAGC	851
Qy	1017	TCCTGCTGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	1076
Db	852	TCCTGCTGCTCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	911
Qy	1077	AGGCCAAAGAAAGAGTTTCAAGATTTTGAAGAAAGAAAGAAAGTCTGAGATGAAA	1136
Db	912	AGGCCAAAGAAAGAGTTTCAAGATTTTGAAGAAAGAAAGAAAGTCTGAGATGAAA	971
Qy	1137	CCCAGACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAAAGAAAGGCCCCGAGACTGTTG	1196
Db	972	CCCAGACAGAGGGGAGCACAGAGAAAGAGATGATGAAGAAAGAAAGGCCCCGAGACTGTTG	1031
Qy	1197	GMAGGAGTGAAGAGCTGACCTCCAGGAGTCACTCTGTTTAAAGAGCTTCAAGAGG	1256
Db	1032	GMAGGAGTGAAGAGCTGACCTCCAGGAGTCACTCTGTTTAAAGAGCTTCAAGAGG	1091
Qy	1257	CTCATACAAAACCTCAGGCAAGCTCAGCTAATGAAGAAAGAGACTTCAAGAAAGTGTGAGG	1316
Db	1092	CTCATACAAAACCTCAGGCAAGCTCAGCTAATGAAGAAAGAGACTTCAAGAAAGTGTGAGG	1151
Qy	1317	CCCTTGAAGGAAATTTCTGCAATTCATCAGAGTTGAATGAAGAAAGAGCTGTTT	1376

Db	1152	CCCTTGAAAGGAAAAATTTGCAATTTCCATTCAGAGTTGAATGAAAAAGCAAGACCTTGT	1211
Qy	1377	ATACTAACAAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAC	1436
Db	1212	ATACTAACAAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAC	1271
Qy	1437	AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACAAAGC	1496
Db	1272	AGGCTAAAAACAGAGGATGAAAGTCCAAATTAATCTGTCTACAGATGACACAAAGC	1331
Qy	1497	TTCTTCAAGAACATAATTAATGCAATTTGAAACCAATTTAGGAACTTAAACAGAAAAAGAGT	1556
Db	1332	TTCTTCAAGAACATAATTAATGCAATTTGAAACCAATTTAGGAACTTAAACAGAAAAAGAGT	1391
Qy	1557	AAAAAGTGGACAGGGCAGTCTGAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAGG	1616
Db	1392	AAAAAGTGGACAGGGCAGTCTGAAGGAACTGAGTGAAGAACTGGAACTGGCAGAGAGG	1451
Qy	1617	CTCTGGCTTCCAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAAGAG	1676
Db	1452	CTCTGGCTTCCAAACAGCTGCAAAATGGAATGAAGCAAAACCATTTGCCAAGCAAGAG	1511
Qy	1677	AGGACCTGGAAACCATGATCCCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC	1736
Db	1512	AGGACCTGGAAACCATGATCCCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTTC	1571
Qy	1737	ATGCTGAAAGAGCAGGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCAATTGCAGC	1796
Db	1572	ATGCTGAAAGAGCAGGAGAGAGAAATTCATGAGGAAAGAGCAACTGGCAATTGCAGC	1631
Qy	1797	TGSCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGGAGGAGGAGTCTTGTATGG	1856
Db	1632	TGSCAGTTCTGCTGAAAGAGAAATGATGCTTTTGAAGACGGAGGAGGAGTCTTGTATGG	1691
Qy	1857	AGATGAGAGTCTGCTGATGGGCGAGAACAAAGTGAATCTGACCAAGAGGCTTACCTGTTTC	1916
Db	1692	AGATGAGAGTCTGCTGATGGGCGAGAACAAAGTGAATCTGACCAAGAGGCTTACCTGTTTC	1751
Qy	1917	AAAGAGGAGCTGAGGACAGGAGTGGCGGCAACAGCGGAAATATTCGGAATTCATTCTGTC	1976
Db	1752	AAAGAGGAGCTGAGGACAGGAGTGGCGGCAACAGCGGAAATATTCGGAATTCATTCTGTC	1811
Qy	1977	CCAAGTGTGGAGAGTCTGCTGATGACATAGACAGTTACAGATTCAGTGAATGGAATGCA	2036
Db	1812	CCAAGTGTGGAGAGTCTGCTGATGACATAGACAGTTACAGATTCAGTGAATGGAATGCA	1871
Qy	2037	TCATTTAAGTGTGATGATACCTCCCTCCCAAACTGTTGCT 2077	
Db	1872	TCATTTAAGTGTGATGATACCTCCCTCCCAAACTGTTGCT 1912	

RESULT 11  
US-10-609-133-13  
; Sequence 13, Application US/10609133  
; Publication No. US20040191798A1  
; GENERAL INFORMATION:  
; APPLICANT: University of Connecticut Health Center  
; APPLICANT: Sarfarazi, Mansoor  
; APPLICANT: Rezaie, Tayebeh  
; TITLE OF INVENTION: Optineurin and Glaucoma  
; FILE REFERENCE: UCT-0046P2  
; CURRENT APPLICATION NUMBER: US/10/609,133  
; PRIOR FILING DATE: 2003-06-26  
; PRIOR APPLICATION NUMBER: 10,281,457  
; PRIOR FILING DATE: 2002-10-25  
; PRIOR APPLICATION NUMBER: 10,090,118  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: 10,060,981  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: 60/344,754  
; PRIOR FILING DATE: 2001-12-24  
; NUMBER OF SEQ ID NOS: 18



Qy 1981 GTGTGGAGAGTCTTGCTGACATAGACAGCTTACAGATTACAGTGTGATGATTGCAATCAT 2040  
Db 1893 GTGTGGAGAGTCTTGCTGACATGACATGACAGCTACAGATTACAGTGTGATGATTGCAATCAT 1952  
Qy 2041 TTAAGTCTGTGATGATACCTCCCAAACTGTTGGT 2077  
Db 1953 TTAGGTGTGATGTGTCACTCCCAAACTGTTGGT 1989  
RESULT 12  
US-10-627-757-1  
; Sequence 1, Application US/10627757  
; Publication No. US20040091914A1  
; GENERAL INFORMATION:  
; APPLICANT: KOUCHI YASUHIRO  
; APPLICANT: MASASGO AKINORI  
; APPLICANT: TAKAHATI TAKAYUKI  
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK  
; FILE REFERENCE: Q76319  
; CURRENT APPLICATION NUMBER: US/10/627,757  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: JP P2002-226612  
; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1734  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-627-757-1  
Query Match 83.3%; Score 1730.8; DB 8; Length 1734;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 1732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 311 ATGTCCCATCAACTCTCAGCTGCTCACTGAAAGAGGACAGCCCGAGTGAAGCACA 370  
Db 1 ATGTCCCATCAACTCTCAGCTGCTCACTGAAAGAGGACAGCCCGAGTGAAGCACA 60  
Qy 371 GGAATGGACCCCGACCTGGCCCAACCCCTGACACAGTTTACCCCGGAGGAGCTG 430  
Db 61 GGAATGGACCCCGACCTGGCCCAACCCCTGACACAGTTTACCCCGGAGGAGCTG 120  
Qy 431 CTGCAGCAGATGAAGAGCTCTGACCAAGAACCCAGCAGCTGAAAGAACCATGAAGCTA 490  
Db 121 CTGCAGCAGATGAAGAGCTCTGACCGAGAACCCAGCAGCTGAAAGAACCATGAAGCTA 180  
Qy 491 AATAATCAAGCCATGAAGAGGAGATTTGAGAGGCTTTGAGAGCTTTGCGCCTGGACAGAGAAACAGAAG 550  
Db 181 AATAATCAAGCCATGAAGAGGAGATTTGAGAGGCTTTGAGAGCTTTGCGCCTGGACAGAGAAACAGAAG 240  
Qy 551 GAAGAACGCCAGTTTGTGATACAGACAGAAAGAACCAAGAGCTCTAATGGCCCTTG 610  
Db 241 GAAGAACGCCAGTTTGTGATACAGACAGAAAGAACCAAGAGCTCTAATGGCCCTTG 300  
Qy 611 AGTCATCAGAAATGAAGAAATGAAGAGAGCTTGGAAACCTTAAAGGGAAATCAGAAAG 670  
Db 301 AGTCATCAGAAATGAAGAAATGAAGAGAGCTTGGAAACCTTAAAGGGAAATCAGAAAG 360  
Qy 671 TCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGAGCGTCTAATGGCCCTTG 730  
Db 361 TCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGAGCGTCTAATGGCCCTTG 420  
Qy 731 GACCAGCTCAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGAGCGTCTAATGGCCCTTG 790  
Db 421 GACCAGCTCAGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGAGCGTCTAATGGCCCTTG 480  
Qy 791 GTGTCTCAACTGACGCTCAAGCTGAACTCCAGCGGCTCCTCAGAGATTCTTTGTTGAA 850  
Db 481 GTGTCTCAACTGACGCTCAAGCTGAACTCCAGCGGCTCCTCAGAGATTCTTTGTTGAA 540  
Qy 851 ATTAGGATGGCTGAAGGAGAGCAGAGGGGTGAGTAAAGAAATCAAGCATAGTCTCTGGG 910

Db 541 ATTAGGATGGCTGAAGGAGAGCAGAGGGTCACTAGTAAAGAAATCAAGCATAGTCTCTGGG 600  
Qy 911 CCCACAGAACAGCTCTCCACTGGCAGCGCATTTCTCTAAATATATAGGAGCAGATCTGCAGAT 970  
Db 601 CCCACAGAACAGCTCTCCACTGGCAGCGCATTTCTCTAAATATATAGGAGCAGATCTGCAGAT 660  
Qy 971 GGGGCCAAGAAATTAATCTTGAACATAGAGGATTAATCTGTGAGCCAGCTCTCTGCTGTGCTTA 1030  
Db 661 GGGGCCAAGAAATTAATCTTGAACATAGAGGATTAATCTGTGAGCCAGCTCTCTGCTGTGCTTA 720  
Qy 1031 AGGGAAGGNAATCAGAAAGCTGGAGAGACTTTGAAGTTGCACTCAAGGAGCCCAAGAAAGA 1090  
Db 721 AGGGAAGGNAATCAGAAAGCTGGAGAGACTTTGAAGTTGCACTCAAGGAGCCCAAGAAAGA 780  
Qy 1091 GTTTTCAGATTTTGAAGAAAGAAACAAGTAACTGTTCTGAGATTGAAATCCCAAGAGGGG 1150  
Db 781 GTTTTCAGATTTTGAAGAAAGAAACAAGTAACTGTTCTGAGATTGAAATCCCAAGAGGGG 840  
Qy 1151 AGCACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGAGACTGTTGGAAGCGAAGTGA 1210  
Db 841 AGCACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGAGACTGTTGGAAGCGAAGTGA 900  
Qy 1211 GCACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAATCTC 1270  
Db 901 GCACTGAACCTCCAGGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAATCTC 960  
Qy 1271 AGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGAGTGTGAGGCCCTTGAAGAGAAA 1330  
Db 961 AGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGAGTGTGAGGCCCTTGAAGAGAAA 1020  
Qy 1331 AATTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTGTTTATATACTAAACAAAAG 1390  
Db 1021 AATTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTGTTTATATACTAAACAAAAG 1080  
Qy 1391 TTAGAGCTCAAGTGGAAGAGCTGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAG 1450  
Db 1081 TTAGAGCTCAAGTGGAAGAGCTGCTATCAGAAATCAAAATGGAACAGGCTTAAACAGAG 1140  
Qy 1451 GATGAAAGTCCAAATTTAACTGTGTACAGTACACACAAACAGCTTCTTCAAGAACAT 1510  
Db 1141 GATGAAAGTCCAAATTTAACTGTGTACAGTACACACAAACAGCTTCTTCAAGAACAT 1200  
Qy 1511 AATAATGCATTTGAAACAAATTCAGGAACTAAACAGAAAGAGAGTCAGAAAAAGTGGACAG 1570  
Db 1201 AATAATGCATTTGAAACAAATTCAGGAACTAAACAGAAAGAGAGTCAGAAAAAGTGGACAG 1260  
Qy 1571 GCAGTCTGAAGAACTGAGTGAAGAACTGGAACTGGCAAGAGAGGCTCTGGCTTCCAAA 1630  
Db 1261 GCAGTCTGAAGAACTGAGTGAAGAACTGGAACTGGCAAGAGAGGCTCTGGCTTCCAAA 1320  
Qy 1631 CAGCTGCAATGATCAAAATGAGCAACCATTTGCCAAGCAGGAGGACCTGGAAACC 1690  
Db 1321 CAGCTGCAATGATCAAAATGAGCAACCATTTGCCAAGCAGGAGGACCTGGAAACC 1380  
Qy 1691 ATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTATGCTGAAAGAGCA 1750  
Db 1381 ATGACCATCTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTATGCTGAAAGAGCA 1440  
Qy 1751 GCAGAGAGAAATTCATGAGGAAAGAGGAGCAATCTGGCAATTCAGCTGGCAGTCTGCTG 1810  
Db 1441 GCAGAGAGAAATTCATGAGGAAAGAGGAGCAATCTGGCAATTCAGCTGGCAGTCTGCTG 1500  
Qy 1811 AAGAGAAATGATGCTTTTGAAGACGAGGAGGAGCTCTTGTGATGAGATGCAAGTCTG 1870  
Db 1501 AAGAGAAATGATGCTTTTGAAGACGAGGAGGAGCTCTTGTGATGAGATGCAAGTCTG 1560  
Qy 1871 CATGGGCGAGAACAAAGTGACTCTGACAGAGGCTTACTCTGTTCAAAGAGAGGCTGAG 1930  
Db 1561 CATGGGCGAGAACAAAGTGACTCTGACAGAGGCTTACTCTGTTCAAAGAGAGGCTGAG 1620  
Qy 1931 GACAGGAGCTGGCGGCAACAGCGGAAATTTCCGATTTCACTTCTGCCCCCAAGTGTGGAG 1990

Db	1621	GACAGGAGCTGGCGGCAACAGCGGAATATTCCGATTCATTCTCTGCCCAAGTGTGGAGAG	1680
Qy	1991	GTTCCTGCTGACATGACACAGCTTTACAGATTTCAGGTGATTCAGTTCGATCATTTAA	2044
Db	1681	GTTCCTGCTGACATGACACAGCTTTACAGATTTCAGGTGATTCAGTTCGATCATTTAA	1734
RESULT 13			
US-10-136-728-71			
; Sequence 71, Application US/10136728			
; Publication No. US20030236188A1			
; GENERAL INFORMATION:			
; APPLICANT: Spytek, Kimberly A.			
; APPLICANT: Li, Li			
; APPLICANT: Edinger, Shlomit R.			
; APPLICANT: Stone, David J.			
; APPLICANT: Guo, Xiaojia			
; APPLICANT: Anderson, David W.			
; APPLICANT: Patturajan, Meera			
; APPLICANT: Gerlach, Valerie L.			
; APPLICANT: Taupier, Raymond J.			
; APPLICANT: Pena, Carol E.A.			
; APPLICANT: Padigar, Muralidhara			
; APPLICANT: Kekuda, Ramesh			
; APPLICANT: Gorman, Linda			
; APPLICANT: Zerhusen, Bryan D.			
; APPLICANT: Smithson, Glenda			
; APPLICANT: MacDougall, John R.			
; APPLICANT: Mezes, Peter S.			
; APPLICANT: Ferman, John A.			
; APPLICANT: Zhong, Mei			
; TITLE OF INVENTION: No. US20030236188A1el Human Proteins, Polynucleotides Encoding Th			
; FILE REFERENCE: 21402-347 D (Cura 647 Other)			
; CURRENT APPLICATION NUMBER: US/10/136,728			
; CURRENT FILING DATE: 2002-05-01			
; PRIOR APPLICATION NUMBER: 60/288,395			
; PRIOR FILING DATE: 2001-05-03			
; PRIOR APPLICATION NUMBER: 60/289,087			
; PRIOR FILING DATE: 2001-05-07			
; PRIOR APPLICATION NUMBER: 60/289,619			
; PRIOR FILING DATE: 2001-05-08			
; PRIOR APPLICATION NUMBER: 60/289,818			
; PRIOR FILING DATE: 2001-05-09			
; PRIOR APPLICATION NUMBER: 60/289,817			
; PRIOR FILING DATE: 2001-05-09			
; PRIOR APPLICATION NUMBER: 60/290,194			
; PRIOR FILING DATE: 2001-05-11			
; PRIOR APPLICATION NUMBER: 60/290,753			
; PRIOR FILING DATE: 2001-05-14			
; PRIOR APPLICATION NUMBER: 60/291,189			
; PRIOR FILING DATE: 2001-05-15			
; PRIOR APPLICATION NUMBER: 60/292,374			
; PRIOR FILING DATE: 2001-05-21			
; PRIOR APPLICATION NUMBER: 60/293,107			
; PRIOR FILING DATE: 2001-05-23			
; Remaining Prior Application data removed - See File Wrapper or PALM.			
; NUMBER OF SEQ ID NOS: 132			
; SEQ ID NO 71			
; LENGTH: 1908			
; TYPE: DNA			
; ORGANISM: Homo sapiens			
; FEATURE:			
; NAME/KEY: CDS			
; LOCATION: (31)..(1714)			
US-10-136-728-71			
Query Match 81.3%; Score 1688.8; DB 7; Length 1908;			
Best Local Similarity 99.6%; Pred. No. 0;			
Matches 1693; Conservative 7; Mismatches 0; Gaps 0;			
Qy	378	GACCCCCCACTGGCGCCACCCAACTGGACACGTTTACCCCGGAGGAGCTGTGCAGC	437

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QY 1518 CATTGAAACAATTGAGGAATAACAAGAAAAGAGTCAGAAAAAGTGGACAGGCAGTGC 1577
Db 1190 CATTGAAACAATTGAGGAATAACAAGAAAAGAGTCAGAAAAAGTGGACAGGCAGTGC 1249
QY 1578 TGAAGGAACAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGC 1637
Db 1250 TGAAGGAACAGTGAAGAACTGGAACTGGCAGAGAGGCTCTGGCTTCCAAACAGCTGC 1309
QY 1638 AAATGGATGAATGAAGCAAAACCAATGCTCAAGCAGGAAGAGGACCTGGAAACCATGACCA 1697
Db 1310 AAATGGATGAATGAAGCAAAACCAATGCTCAAGCAGGAAGAGGACCTGGAAACCATGACCA 1369
QY 1698 TCCTCAGGCTCAGATGAAGTTTACGTCTCTGATTTTCAATGCTGAAAGAGCAGGAG 1757
Db 1370 TCCTCAGGCTCAGATGAAGTTTACGTCTCTGATTTTCAATGCTGAAAGAGCAGGAG 1429
QY 1758 AGAAATTCATGAGGAAAGAGCAACTGGCAATGCGAGCTGGCAGTCTCTGTAAGAGA 1817
Db 1430 AGAAATTCATGAGGAAAGAGCAACTGGCAATGCGAGCTGGCAGTCTCTGTAAGAGA 1489
QY 1818 ATGATGCTTTGAAAGCAGGAGCAGGAGTCTTGTGATGGAGATGCAGAGTCGTCAATGGG 1877
Db 1490 ATGATGCTTTGAAAGCAGGAGCAGGAGTCTTGTGATGGAGATGCAGAGTCGTCAATGGG 1549
QY 1878 CGAACAAGTGAATCTGACAGCAGGCTTACCTTGTTCATGCTGAAAGAGGAGTGAAGCAGG 1937
Db 1550 CGAACAAGTGAATCTGACAGCAGGCTTACCTTGTTCATGCTGAAAGAGGAGTGAAGCAGG 1609
QY 1938 ACTGGCGCACACGCGAATATTCGATTCATCTCTGCTCCCAAGTGGAGAGTCTTGC 1997
Db 1610 ACTGGCGCACACGCGAATATTCGATTCATCTCTGCTCCCAAGTGGAGAGTCTTGC 1669
QY 1998 CTGACATAGACACCTTACAGATTCACCTGATGATTCATCTTAAAGTGTGATGATC 2057
Db 1670 CTGACATAGACACCTTACAGATTCACCTGATGATTCATCTTAAAGTGTGATGATC 1729
QY 2058 ACTTCCCAAAACTGTGGT 2077
Db 1730 ACTTCCCAAAACTGTGGT 1749
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## RESULT 14

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US-10-136-728-69
; Sequence 69, Application US/10136728
; Publication No. US20030236188A1
; GENERAL INFORMATION:
; APPLICANT: Spytex, Kimberly A.
; APPLICANT: Li, Li
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Stone, David J.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Anderson, David W.
; APPLICANT: Patturajan, Meera
; APPLICANT: Gerlach, Valerie L.
; APPLICANT: Taupier, Raymond J.
; APPLICANT: Pena, Carol E.A.
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Gorman, Linda
; APPLICANT: Zerhusen, Bryan D.
; APPLICANT: Smithson, Glenda
; APPLICANT: MacDougall, John R.
; APPLICANT: Mezes, Peter S.
; APPLICANT: Perman, John A.
; APPLICANT: Zhong, Mei
; TITLE OF INVENTION: No. US20030236188A1el Human Proteins, Polynucleotides Encoding TH
; FILE REFERENCE: 21402-347 D (Cura 647 Other)
; CURRENT APPLICATION NUMBER: US/10/136,728
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/288,395
; PRIOR FILING DATE: 2001-05-03
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; PRIOR APPLICATION NUMBER: 60/289,087
; PRIOR FILING DATE: 2001-05-07
; PRIOR APPLICATION NUMBER: 60/289,619
; PRIOR FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: 60/289,818
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/289,817
; PRIOR FILING DATE: 2001-05-09
; PRIOR APPLICATION NUMBER: 60/290,194
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: 60/290,753
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: 60/291,189
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/292,374
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/293,107
; PRIOR FILING DATE: 2001-05-23
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 69
; LENGTH: 1908
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (31)..(1714)
US-10-136-728-69
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Query Match 79.3%; Score 1646.6; DB 7; Length 1908;
Best Local Similarity 98.5%; Pred. No. 0;
Matches 1674; Conservative 0; Mismatches 7; Indels 18; Gaps 1;
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QY 379 ACCCCCCACCTCGGCCACCCCAACCTGGACACGTTTACCCCGGAGGAGCTGTCGACGA 438
Db 69 ATCCTCCCACCTGGATCTCCCAAACTGGACACATTTACCCCGGAGGAGCTGTCGACGA 128
QY 439 GATGAAAGAGCTCCTGACCAAGAAACCAACAGCTGAAAGAGCCATGAAGCTAAATATCA 498
Db 129 GATGAAAGAGCTCCTGACCGAGAACCAACAGCTGAAAGAGCCATGAAGCTAAATATCA 188
QY 499 AGCCATGAAAGGAGATTTGAGGAGCTTTCGGCTCGACAGAGAAACAGAGAAAGAAACG 558
Db 189 AGCCATGAAAGGAGATTTGAGGAGCTTTCGGCTCGACAGAGAAACAGAGAAAGAAACG 248
QY 559 CCAGTTTTTTTGATACAGAGCAAGCAAGCAAGAGCGCTTAATGCGCTTGAGTCATGA 618
Db 249 CCAGTTTTTTTGATACAGAGCAAGCAAGCAAGAGCGCTTAATGCGCTTGAGTCATGA 308
QY 619 GAATGAGAAATTGAAGGAGAGCTTGGAAAACTTAAAGGGAAATCAGAAAGGTCACTCTGA 678
Db 309 GAATGAGAAATTGAAGGAGAGCTTGGAAAACTTAAAGGGAAATCAGAAAGGTCACTCTGA 368
QY 679 GGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGCGGAGCAGAGAAAGACAGCT 738
Db 369 GGACCCCACTGATGACTCCAGGCTTCCAGGGCCGAGCGGAGCAGAGAAAGACAGCT 428
QY 739 CAGGACCCAGGTGGTGAGGCTACAGCAGAGAGGAGCAGACCTGTTGGGCATCGTGTCTGA 798
Db 429 CAGGACCCAGGTGGTGAGGCTACAGCAGAGAGGAGCAGACCTGTTGGGCATCGTGTCTGA 488
QY 799 ACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATTCTCTTTGTTGAAATTAGGAT 858
Db 489 ACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAAAGATTCTCTTTGTTGAAATTAGGAT 548
QY 859 GGCTGAAGGAGAGCAAGAGGCTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCCAACGAG 918
Db 549 GGCTGAAGGAGAGCAAGAGGCTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCCAACGAG 608
QY 919 AACAGTCTCCACTGGCAGCGGATTTGCTAAATATAGGAGCAGATCTGACAGATGGGCCCAA 978
Db 609 AACAGTCTCCACTGGCAC-----GAGCAGATCTGCAGATGGGCCCAA 650
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Qy	383	CCCACCTGGCCCAACCCAAACCTCGACACAGTGTAAACCCCGGAGGAGCTGCTGCACGAGATG	442
Db	223	TCCAATATGGTTTCAACCCAGCCTCGACACATTTCAACCCCTGAGGAGCTGCTGCACGAAATG	282
Qy	443	AAAGAGTCTCTGACCAAGAACCCACAGCTGAAGACCAATGAAGCTTAAATAATCAAGCC	502
Db	283	AAGAACTCTCTGGTTGAAACCAACAGCTGAAGAGCCATGAAGCTTAAATAATCAAGCT	342
Qy	503	ATGAAAGGAGATTTGAGGAGCTTTTCGGCCTTGGACAGAGAAACAGAAAGGAGAAACGCGCAG	562
Db	343	ATGAAAGGCGATTTGAGGAGCTGTCCGCTTGGACAGAGAAAGGAGAGAGCGCCTG	402
Qy	563	TTTTTTGAGATACAGAGCAAAAGACAGAGCGTCTAATGCGCTTGAAGTCATGAGAT	622
Db	403	TTGTTTGAGATGCAAGCAAAAGAGGTTAAGGAGCGCCTTAAGGCGCTGACTCATGAAAT	462
Qy	623	GAGAAATTTGAAGGAAGAGCTTTGGAATACTAAAGCGGAAATCAGAAAGGTCATCTGAGGAC	682
Db	463	GAGAGGCTGAAGGAAGAGCTTTGGAATTTCAAGAGAAATCAGAAAGCCATTTGGAAGAC	522
Qy	683	CCCACTGATGATCTCAGGCTTTCCAG-----GGCC	712
Db	523	CTCACAGTGGCTACAGGTATCCACAGAGCCTTGGAGGAGGAAGTGAGAGACTGAAGACC	582
Qy	713	GAAGCGAGACGAAAGAGGACCACTCAGGACCCAGGTGGTGAGGCTACAAAGCAGAGAAG	772
Db	583	CAGGTGAGCAGGAAGTGGAGCATCTGAAGATCCAGGTGATGCCCTTCGGGCTGAAAG	642
Qy	773	GCAGACTGTTGGGCATCTGTCTGAATCGCAGCTCAAGCTGAAGCTCCAGCGGCTCCCTCA	832
Db	643	GCAGCTGCTGGGCATCTGTCTCAGAACTGCGAGCTCAAACTCAACTTCGGCGGCTCCTCG	702
Qy	833	GAAGATTCCTTTGTTTGAATTTAGGATGGCTGAAGGAGAAAGCAGAAAGGTCAGTAAAAAGAA	892
Db	703	GAAGACTCCTTCGTTGAGATCAGATGACCGAAGGAGAGACTGAAGGGCCATGAGAGAG	762
Qy	893	ATCAAGCATATGTCCTGGGCCCAACGAGAACAGTCTTCCACTGGCAGCGCATTTGTCATAATAT	952
Db	763	ATGAAGAACTGCCCTACACCCACAAGAACACAGACCCCATCAGC-----	804
Qy	953	AGGAGCAGATCTGAGATGGGCCCAAGATTAATCTTCGAAATGAGGAGTTAACTGTGAGC	1012
Db	805	TTGAGCAACTGTACAGAGGATGCCAGAGATTGTGCGGAGTTTGAAGAACTGACTGTGAGC	864
Qy	1013	CAGCTCTCTGTCTGCCCTAAGGGAAGGGAATCAGAAAGGTGGAGAGACTTTGAAGTTGCACTC	1072
Db	865	CAGCTTCTGTCTTGGCTTAAGGGAAGGAAACCAAAAGGTGGAGAGACTTTGAAGTCGCCCTC	924
Qy	1073	AAGGAGCCAAAGAAAGAGTTTCAGATTTTGAAGAAGAAACAGATTAATCTGTTCTGAGATT	1132
Db	925	AGAGAACCAGAAAGAAAGAAATTTTCAGATTTTGAAGAAGAAAGCAATGGCCATTTCTTCTACT	984
Qy	1133	GAACCCAGACAGAGGGGAGCAGAGAAAGAGATGATGAGAGAAAGGCCCGGAGACT	1192
Db	985	GAGAAGCAGACAGCGAGGAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT	1041
Qy	1193	GTTTGAAGCGAAGTGAAGCACTGAACTCCAGTGTGACATCTCTGTTTAAAGGAGCTTCAA	1252
Db	1042	GTTTGAAGCGAGTGGAAACACTGAGGATTTCAAGTGACCTCTCTGTTTAAAGGAGCTTCAA	1101
Qy	1253	GAGCTCATACAAACTCAGCGAAGCTGAGCTAATGAAGAGAGAGACTTCAAGAAAGTGT	1312
Db	1102	GAGGCACACAAACTCAGTGAGGCTGAGCTGATGAAGAGAGACTTCAAGAAAGTGT	1161
Qy	1313	CAGGCCCTTGAAGGAAAGATTTCTGCAATTTCCATCAGAGTTGAATGAAAGCAGAGACTT	1372
Db	1162	CAGGCTCTGAGAGGAAAGAACTCTGCAACCACTCAGAGCTGATGAAAGCAGAGAGCTC	1221
Qy	1373	GTTTATACTAACAAAAAGTTAGAGCTACAGTGGAAAGAGCTATTCAGAGAAATCAAAGT	1432
Db	1222	GTTTACGTAACAAAGATTTAGAGCTCAGGTGGAGAGCAGTCCGCTCCGAAATCAAGATG	1281
Qy	1433	GAACAGGCTAAAAACAGAGGATGAAAGCTCCAAATTAATCTGTGCTACAGATGACACACAAC	1492

[illegible]

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RESULT 18
US-10-609-133-15
; Sequence 15, Application US/10609133
; Publication No. US20040191798A1
; GENERAL INFORMATION:
; APPLICANT: University of Connecticut Health Center
; APPLICANT: Sarfarazi, Mansoor
; APPLICANT: Rezaie, Tayebbeh
; APPLICANT: Child, Anne H
; TITLE OF INVENTION: Optineurin and Glaucoma
; FILE REFERENCE: UCT-0046P2
; CURRENT APPLICATION NUMBER: US/10/609,133
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: 10,281,457
; PRIOR FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 10,090,118
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: 10,060,981
; PRIOR FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: 60/344,754
; PRIOR FILING DATE: 2001-12-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15
; LENGTH: 1787
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM 145081

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; DATABASE ENTRY DATE: 2003-04-06  
; RELEVANT RESIDUES: (1)..(1787)  
US-10-609-133-15

Query Match 50.9%; Score 1057; DB 9; Length 1787;  
Best Local Similarity 77.7%; Pred. No. 9.7e-282;  
Matches 1396; Conservative 0; Mismatches 330; Indels 71; Gaps 7;

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QY 297 CAGGAATCTTCTGCAATGTCCTCACTCAACCTCTCAGCTGCTCACTGAAAGGAGGACAGCC 356
DB 13 CCGGACCTGTTACATGTCCTCAACCTCTGAGCTGCTGACTGAAAGGGGAGAGCT 72
QY 357 CCAGTGAAAGCAGGAAATGACCCGCCACCTGGCCACCCCAACCTGGACACGTTTA 416
DB 73 CCGTGAGAGCCCGAGAAATGACCCCTCCAAATGCTTCAACCCCAACCTGGACACATTC 132
QY 417 CCGCGAGAGCTGCTGACGAGATGAAAGAGCTCTGACCAAGAACCAACGAGCTGAAAG 476
DB 133 CTCCTGAGGAGCTGCTGACGCAAAATGAAAGAACTCTGGTCGAGAACCAACGAGCTGAAAG 192
QY 477 AAGCCATGAAGCTTAATATCAAGCCATCAAGGGAGATTTGAGGAGCTTTCGGCTGGA 536
DB 193 AAGCCATGAAGCTTAATATCAAGCTATGAAGGGGCTTTGAGGAGCTTTCGGCTGGA 252
QY 537 CAGAGAAAACAGAGGAAGAACGCGCAGTTTTTTTGGATACAGAGCAAGAAAGCAAGAGC 596
DB 253 CAGAGAGCGAGAGGAAGAACGCGCAGTTGTTGAGATACAGAGCAAGAAAGAGGCTAAGGAGC 312
QY 597 GTCTAATGCGCTTGAGTCATGAGATGAGAAATTTGAAGGAAGAGCTTGGAAACTTAAAG 656
DB 313 GCCTCAAGGCCCTGAGTCATGAAATGAGAGGCTGAAGGAAGAGCTTGGAAACTTAAAG 372
QY 657 GGAATTCAGAAAGCTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAGGGCG --- 713
DB 373 AGAAATCAGAAAGGCCATTTGAAGACATCAGAGTAGATGCGGTTTTCCAGAACCGACT 432
QY 714 -----AAGCGGAGCAGGAAAGGACCAGCTCAGG 742
DB 433 TGGAGCAGGAAGTGGGAGCAACTGAAGAGCGAGGTGAGCAGGAAGTGGAGCATCTGAAG 492
QY 743 ACCAGGTGGTGAAGCTTACAGC ---AGAGAGGCGAGACCTGTGGGCACTGCTGTCTGAA 799
DB 493 ATCCAGGTGAGGCGCTTCAGGCTTGAGAAAGCGGACCTTGCTGGGGCAATTCGTCTCAGA 552
QY 800 CTGACGCTCAAGCTGAACCTCAGCGGCTCTCAGAGAGATTCCTTTCTGAAATTAGGATG 859
DB 553 CTGACGCTCAGGCTCAACTCCGCGGCTCTCAGAAAGACTCTCTGTTGGAGA -CAGGATG 611
QY 860 GCTGAAGGAGAGCAGAGGGGTGAGTAAAGAAATCAAGCATAGTCTCGGGCCCAACGAGA 919
DB 612 ACTGAAGGAGAGCGGAGAGGGGCAATGAAGGAGATGAGGAAACAGCGCTGGACCCCAAGG 671
QY 920 ACAGTCTCAGCTGGGACCGGATTTGCTAAATATAGAGCAGATCTCGCAGATGGGGCCAAG 979
DB 672 ACAGACTCCATCATCTGG -----GCAAAATGTACAGAGGACGCGCAGG 713
QY 980 AATTACTTCGAACATCAGAGGTAACTGTGAGCCAGCTCTGCTGTGCTTAAGGGAAGG 1039
DB 714 ACTTGTGTGAGTTTGAAGAACTGACTGTGAGGCAACTCTGCTTTGCTTCAGGGAAGGA 773
QY 1040 AATCAGAAGGTGAGAGACTTGAAGTTGCACTCAAGGAGGCCCAAGAAAGAGTTTTCAGAT 1099
DB 774 AACCAGAAAGGTGAGAGACTCGAGATCGCGCTCAGAGAGGCCAAGAAAGAAATTTTCAGAT 833
QY 1100 TTTGAAAGAAACAAAGATTAATGCTTCTGAGATTTGAAACCCAGACAGAGGGGAGCAGAG 1159
DB 834 TTTGAAAGAAAGCAACCGGCCATTTCTGCGATTTGAAACCCAGACAGAGGGGAGCAGACAA 893
QY 1160 AAGAGAAATGATGAACAGAAAGGCCCGGAGACTGTTTGAAGCGAAGTGAAGCACTGAAC 1219
DB 894 AAG ---AGAGGAGAGCAAGAGCCAGAGAGTGTGGGAATCGAAGTGGAAATCTTGAAC 950
QY 1220 CTCAGGTCACATCTCTGTTTAAAGGAGCTTCAAGAGGCTCATCAAAACTCAGCGAAGCT 1279
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DB 951 GTTCAAGTGGCCTCTCTGTTTAAAGGGCTTCAAGAGGCGCACACAAAGCTCAGTGAGGCC 1010
QY 1280 GAGCTAATGAAAGAGACTTCAAGAAAGTCTCAGGCCCTTGAAGGAAATTTCTGCA 1339
DB 1011 GAGCTGATGAAGAGAGACTTCAAGAAAGTCTCAGGGCTCTGGAAGGAGAACTCTGCA 1070
QY 1340 ATTCCATCAGAGCTTCAATGAAAGCAAGAGCTTGTTTATCTAAACAAAGTTTAGAGCTA 1399
DB 1071 ACCCATCGAGCTGAATGAAGCAAGAGCTCGTTTACAGTAACTGGAGTTTAGAGCTG 1130
QY 1400 CAAAGTGAAGCATCTATCAGAAATCAAAATGGAACAGGCTAAACACAGAGGATGAAAG 1459
DB 1131 CAGGTGGAGAGCATCGCTCGGAAATCAAGATGGAGCGCCCAAGACAGAGGAGGAGAA 1190
QY 1460 TCCAAATTAATGCTGTCTACAGATGACACACAAAGCTTCTTCAAGAAATATAATGCA 1519
DB 1191 TCCAGGTTTAGCCACTCTTCAGGCAACACACGAAAGCTCTTTCAGGAAACAAATAAAGCT 1250
QY 1520 TTGAAAAACAATTGAGGAACTAAACAGAAAGAGTCAAGAAAAAGTGGACAGGGCAGTCTG 1579
DB 1251 CTGAGAACAAATTGAAGAACTAACCAACACAGGCGAAGAAAGTGGACAGGTGACAGCTG 1310
QY 1580 AAGGAATGAGTGAAGAACTGGAACCTGGCAGAGAAAGGCTCTGCTTTCCAAACAGCTGCAA 1639
DB 1311 CAGGAGCTCAGCGAGAGCTGGAGCTGGCGGAGCAGGCTCTGGCGTCCAAGCAGCTCCAG 1370
QY 1640 ATGGATGAATCAAGCAACCACTGCCAAGCAGGAGAGGAGCTTGAAGACCATGACCATC 1699
DB 1371 ATGGATGAGATGAAGCAGACCATGCCAAGCAGGAGGAGGAGCTTGAGACCATGGCGCTC 1430
QY 1700 CTCAGGCTCAGATGGAAGTTTACTGTTCTGATTTTCTGCTCAAAAGAGCAGCGAGAGAG 1759
DB 1431 CTCAGGCTCAGATGGAAGTGTACTGTTTCAAGTTCCTGCTGAGAGGCGAGCAAGGAG 1490
QY 1760 AAAATTCTAGAGAAAGAGCAACTGGCAATTCAGCTGGCAGTTCCTGCTGAAAGAGAAAT 1819
DB 1491 AAGATCCATGAGAAAGAGCAGCTGGCTTTCGACTGCCATTTTGTGTAAGAGAAAC 1550
QY 1820 GATGCTTTCGAAGACGAGGC ---AGGCAGTCTTGTATGAGATGAGATGAGATGCTGATGGG 1876
DB 1551 AATGACTTTGAAGATGAGGCGAGTGGCAGTCTTGTATGAAATGAGTGCCTGGCAGCGG 1610
QY 1877 GCGAGAACAAAGTGACTCTGACCGAGAGGCTTACCTTTGTTTCAAAGAGGAGCTGAGACAGG 1936
DB 1611 GCGAGAACCGAGCACTGACCGAGAGGCTTACCTGTTTCAAAGAGGAGCCAGGACATG 1670
QY 1937 GACT-----GGCGCAACAGCGGAATATTCGATTCATTCCTGCCCCCAAGTGTGGA 1987
DB 1671 AGCTGGCAGCATGGGCGAGCAGCGCCCGAGTATTTCCATTTCACTGCTGCCCCCAAGTGTGG 1730
QY 1988 GAGGTTCTGCTGACATAGACAGCTTACAGATTCAGTGTGATGATTCATTTAA 2044
DB 1731 GAGGCTCTCGCGGACATTCAGACGCTTACAGATACATGTATGACTGTATCTCTGA 1787
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RESULT 19  
US-10-779-543-5625  
; Sequence 5625, Application US/10779543  
; Publication No. US2005022791A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams et al  
; TITLE OF INVENTION: GENE PRODUCTS DIFFERENTIALLY EXPRESSED  
; TITLE OF INVENTION: IN CANCEROUS CELLS AND THEIR METHODS OF USE II  
; FILE REFERENCE: 2300-21302  
; CURRENT APPLICATION NUMBER: US/10/779,543  
; CURRENT FILING DATE: 2004-02-12  
; PRIOR APPLICATION NUMBER: 10/076,555  
; PRIOR FILING DATE: 2002-02-15  
; PRIOR APPLICATION NUMBER: 09/217,471  
; PRIOR FILING DATE: 1998-12-21  
; PRIOR APPLICATION NUMBER: 60/068,755  
; PRIOR FILING DATE: 1997-12-23







QY 1136 ACCCAGACAGAGGGAGCAGACAGAGAAAGAGATGATGAGAGAAAGGCCCGGAGACTGTT 1195  
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Db 181 ACCCAGACAGAGGAGCAGACAGACAGAGAAAGAGAGAGAGAGACACCAAACTATT 240  
QY 1196 GGAAGCAAGTGAAGCACTGAACCTTCAGGTGACATCTCTGTTAAAGGAGCTTCAAGAG 1255  
241 GGAAGTGAAGTGAAGCACTGAACCTTCAGGTGACAACTCTGTTAAAGGAGCTTCAGGAA 300  
QY 1256 GCTCATACAAAACCTCAGCAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAGTGTGAG 1315  
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Db 301 GCTCACACAAAACCTCAGTGAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAGTGTGAG 360  
QY 1316 GCCCTTGAAGAAAATCTGCAATTCATCAGAGTTCAATCAAAAAGCAAGAGCTTGT 1375  
361 GCCCTTGAAGAAAATCTGCAAGCTGAGCTTAATGAAGAGAGACTTCAAGAAAAGTGTGTT 420  
QY 1376 TATACTAACAAAAG 1390  
|||||  
Db 421 TATAAAAACAAAAG 435  
RESULT 25  
US-09-960-352-14434  
; Sequence 14434, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 14434  
; LENGTH: 416  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 62-BOVMS1-017-Q1-E1-H10  
US-09-960-352-14434  
Query Match 16.1%; Score 333.4; DB 3; Length 416;  
Best Local Similarity 87.7%; Pred. No. 2.5e-81;  
Matches 364; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 1001 TTAACCTGTGAGCGAGCTCTGCTGCTTAAGGAAAGGAATCAGAAAGGTGAGAGACTT 1060  
Db 2 TTAACCTGTGAGCGAGCTCTGCTGCTTAAGGAAAGGAATCAGAAAGGTGAGAGACTT 61  
QY 1061 GAAGTTGCACTCAAGAGAGCCCAAGAAAGTTTCAGATTTTGAAGAAAGAAACAGTANT 1120  
62 GAAGTTGCCCTCAAGGAAGCCCAAGAAAGAAATTTCTGATTTTGAAGAAAGAAAGCAAGGAT 121  
QY 1121 CGTTCTGAGATTGAACCCAGACAGAGGGGAGCAGACAGAAAGAGATGATGAAGAGAAA 1180  
Db 122 CATCTGAGACTGAGACCCAGACAGAGGGAGCAGACAGACAGAAAGAGAGAGAGAAA 181  
QY 1181 GGGCCCGAGACTGTTGGAGCGAAGTGGAGAGCACTGAACTCCAGGTGACATCTCTGTTT 1240  
Db 182 GACACCAAAACTATTGGAAGTGAAGTGAAGAACTGAACTGAACTGAGTGACAACTCTGTT 241  
QY 1241 AAGGAGCTTCAAGAGCTCATACAAACTCAGGAGCTGAGCTAATGAAGAGACTT 1300  
Db 242 AAGGAGCTTCAAGAGCTCAGCAAACTCAGTGAAGCTGAGCTAATGAAGAGACTT 301  
QY 1301 CAAGAAAAGTGTGAGGCCCTTGAAGAGAAAATTTCTGCAATTCATCAGAGTTGAATGAA 1360  
Db 302 CAAGAAAATGTGAGGCCCTTGAAGAGAAAATTTCTGCAAGCCCATCAGAACTGAATGAA 361  
QY 1361 AAGCAAGAGCTTGTATTACTACAAAAGTTAGAGCTACAGTGAAGAGCATGC 1415  
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Db 362 AAACAAGAGCTGGTTTATATAAAAAACAAAAGTTAGAGCTCAAGTGAAAGCATGC 416  
RESULT 26  
US-11-060-867-55  
; Sequence 55, Application US/11060867  
; Publication No. US20050239146A1  
; GENERAL INFORMATION:  
; APPLICANT: Tainsky, Michael  
; APPLICANT: Draghici, Sorin  
; APPLICANT: Chatterjee, Madhumita  
; TITLE OF INVENTION: Neopeptide Detection of Disease Using Protein Arrays  
; FILE REFERENCE: 0788.00067  
; CURRENT APPLICATION NUMBER: US/11/060,867  
; CURRENT FILING DATE: 2005-02-17  
; PRIOR APPLICATION NUMBER: US 10/004,587  
; PRIOR FILING DATE: 2001-12-04  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 364  
; TYPE: DNA  
; ORGANISM: homo sapien  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (242)..(242)  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (253)..(253)  
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (264)..(264)  
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; LOCATION: (284)..(284)  
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; OTHER INFORMATION: n is a, c, g, or t  
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; LOCATION: (301)..(301)  
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; LOCATION: (305)..(305)  
; OTHER INFORMATION: n is a, c, g, or t  
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (313)..(313)  
; OTHER INFORMATION: n is a, c, g, or t  
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; NAME/KEY: misc\_feature



LOCATION: (322)..(322)  
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OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (327)..(327)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (332)..(332)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (335)..(335)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (340)..(340)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (346)..(346)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (350)..(350)  
OTHER INFORMATION: n is a, c, g, or t  
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NAME/KEY: misc feature  
LOCATION: (357)..(357)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (359)..(361)  
OTHER INFORMATION: n is a, c, g, or t  
US-11-060-867-55

Query Match 15.9%; Score 330; DB 13; Length 364;

Best Local Similarity 93.0%; Pred. No. 2e-80;  
Matches 330; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 979 GAATTACTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCCTGCTGCTTAAGGGAAGG 1038  
Db 10 GAATTACTTCGAACATGAGGAGTTAACTGTGAGCCAGCTCCTGCTGCTTAAGGGAAGG 69  
QY 1039 GAATCAGAGGTGAGGAGCTTGAAGTTGCACTCAAGGAGCCCAAGAAAGAGTTTCAGA 1098  
Db 70 GAATCAGAGGTGAGGAGCTTGAAGTTGCACTCAAGGAGCCCAAGAAAGAGTTTCAGA 129  
QY 1099 TTTTGAAGAAAGAAAGTAACTGCTGAGATTGAAACCCAGACAGAGGGGAGCACAGA 1158  
Db 130 TTTTGAAGAAAGAAAGTAACTGCTGAGATTGAAACCCAGACAGAGGGGAGCACAGA 189  
QY 1159 GAAAGAGAAATGATGAAGAGAAAGCCCGGAGACTTTGGAAGCGAAGTGAAGCACTGAA 1218  
Db 190 GAAAGAGAAATGATGAAGAGAAAGCCCGGAGACTTTGGAAGCGAAGTGAAGCACTGAA 249  
QY 1219 CCTCCAGGTACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGC 1278  
Db 250 CCTNCAAGGTACATNTGTTTAAGGAGCTTNAANAGGCTNATACAAAACCTNANCNAAC 309  
QY 1279 TGAGCTAAATGAAGAGAGACTTCAAGAAAGTGTGAGGCCCTTGAAGGAAAT 1333  
Db 310 TGANCTAATGAANAANAANACTTNAANAANAANTGTNANGCCNTTGAAGANNNAAT 364

RESULT 27

US-09-918-995-7614  
; Sequence 7614, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: Fast-Seq for Windows Version 3.0  
; SEQ ID NO 7614  
; LENGTH: 432  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-7614

Query Match 14.3%; Score 296.2; DB 3; Length 432;  
Best Local Similarity 99.0%; Pred. No. 5.4e-71;  
Matches 298; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 298 AGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAGGAGGACAGCCC 357  
Db 130 AGGAACCTTCTGCAATGTCCCATCAACCTCTCAGCTGCCTCACTGAAAGGAGGACAGCCC 189  
QY 358 CAGTGAAGCACAGGAAATGGACCCGCCACCTGGGCCACCCAACTGGACACGTTTAC 417  
Db 190 CAGTGAAGCACAGGAAATGGACCCGCCACCTGGGCCACCCAACTGGACACGTTTAC 249  
QY 418 CCGGAGGAGCTGCTGCAGCAGATGAAGAGCTCTCAGCAGAACCCAGAGCTGAAAGA 477  
Db 250 CCGGAGGAGCTGCTGCAGCAGATGAAGAGCTCTCAGCAGAACCCAGAGCTGAAAGA 309  
QY 478 AGCCATGAAGCTAAATAATCAAGCCATGAAGGAGAGATTTCAGGAGCTTTCCGGCTGGAC 537  
Db 310 AGCCATGAAGCTAAATAATCAAGCCATGAAGGAGAGATTTCAGGAGCTTTCCGGCTGGAC 369  
QY 538 AGAAGAACAGAGAGAGAGCCAGCTTTTGTGATGATACAGAGCAAGCAAGAGAGCG 597  
Db 370 AGAAGAACAGAGAGAGAGCCAGCTTTTGTGATGATACAGAGCAAGCAAGAGAGCG 429  
QY 598 T 598  
Db 430 T 430

RESULT 28

US-11-128-061-2706  
; Sequence 2706, Application US/11128061  
; Publication No. US20060003958A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
; FILE REFERENCE: 01997.027701  
; CURRENT APPLICATION NUMBER: US/11/128,061  
; CURRENT FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; PRIOR FILING DATE: 2004-05-11  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2706

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; LENGTH: 505
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-2706

Query Match      14.1%; Score 292.4; DB 16; Length 505;
Best Local Similarity 80.8%; Pred. No. 6.6e-70;
Matches 341; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 289 CTTTCCACAGAACTTCTGCAATGTCCCATCAACTCTCAGCTGCCTCACTGCAAAAGGA 348
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
83 CTAAGCCGACGACCTGTTACCATGTCCCATCAACTCGAGCTGCCTGACTGAGNAGGG 142
QY 349 GGACAGCCCCAGTGAAGACACAGGAAATGGACCCCCACCTGGCCCCACCCAAACCTGGA 408
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 TGACAGCCTCTGTGAGACCCGAGGAAATGAACCCCTTAATAAGGTTTCAACCCAGCCTGGA 202
QY 409 CACGTTTACCCGAGGAGCTGCTCAGCAGATGAAGAGCTCTCGACCAAGAACCA 468
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 CACATTCTCTCTGAGGAGTCTGCAGCAATGAAGGAACCTCTGGTTGAGAACCA 262
QY 469 GCTGAAAGAGCCATGAAGTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTC 528
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
263 GCTGAAAGAGCCATGAAGTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTC 322
QY 529 GGCCTGGACAGAAACAGAGGAAAGAGGAAAGAGTCTCTGACCAAGAACCA 468
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 CACATTCTCTCTGAGGAGTCTGCAGCAATGAAGGAACCTCTGGTTGAGAACCA 262
QY 469 GCTGAAAGAGCCATGAAGTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTC 528
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
263 GCTGAAAGAGCCATGAAGTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTC 322
QY 529 GGCCTGGACAGAAACAGAGGAAAGAGGAAAGAGTCTCTGACCAAGAACCA 468
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
323 AGCCTGGCAGAGAGCAGAGGAAAGAGGAAAGAGTCTCTGACCAAGAACCA 382
QY 589 AAAAGAGCGTCTAATGGCCTTGAGTCATGAGAAATGAAGGAAAGAGCTTGGAAA 648
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
383 TAAGAAGCTCTGATGACCTTGAGTTATGAAATGAAGAACTGAAGTGAGCTTGGAAA 442
QY 649 ACTAAAGGGAATCAGAAGGTCATCTGAGACCCACTGATGACTCCAGGCTCCAG 708
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
443 ACTAAGAGAGAGTCAGAAAGGCCATTTGAAGGCTCCATATGTGGCTCCAGGCTCCCAT 502
QY 709 GG 710
Db      |||
503 GG 504
```

```
RESULT 29
US-11-128-061-6348
; Sequence 6348, Application US/11128061
; Publication No. US2006003958A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS
; FILE REFERENCE: 01997.027701
; CURRENT APPLICATION NUMBER: US/11/128,061
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6348
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-061-6348

Query Match      14.1%; Score 292.4; DB 16; Length 505;
Best Local Similarity 80.8%; Pred. No. 6.6e-70;
Matches 341; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
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```
QY 289 CTTTCCACAGAACTTCTGCAATGTCCCATCAACTCTCAGCTGCCTCACTGCAAAAGGA 348
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
83 CTAAGCCGACGACCTGTTACCATGTCCCATCAACTCGAGCTGCCTGACTGAGNAGGG 142
QY 349 GGACAGCCCCAGTGAAGACACAGGAAATGGACCCCCACCTGGCCCCACCCAAACCTGGA 408
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 TGACAGCCTCTGTGAGACCCGAGGAAATGAACCCCTTAATAAGGTTTCAACCCAGCCTGGA 202
QY 409 CACGTTTACCCGAGGAGCTGCTCAGCAGATGAAGAGCTCTCGACCAAGAACCA 468
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
203 CACATTCTCTCTGAGGAGTCTGCAGCAATGAAGGAACCTCTGGTTGAGAACCA 262
QY 469 GCTGAAAGAGCCATGAAGTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTC 528
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
263 GCTGAAAGAGCCATGAAGTAAATCAAGCCATGAAGGAGATTTGAGAGCTTTC 322
QY 529 GGCCTGGACAGAAACAGAGGAAAGAGGAAAGAGTCTCTGACCAAGAACCA 468
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
323 AGCCTGGCAGAGAGCAGAGGAAAGAGGAAAGAGTCTCTGACCAAGAACCA 382
QY 589 AAAAGAGCGTCTAATGGCCTTGAGTCATGAGAAATGAAGGAAAGAGCTTGGAAA 648
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
383 TAAGAAGCTCTGATGACCTTGAGTTATGAAATGAAGAACTGAAGTGAGCTTGGAAA 442
QY 649 ACTAAAGGGAATCAGAAGGTCATCTGAGACCCACTGATGACTCCAGGCTCCAG 708
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
443 ACTAAGAGAGAGTCAGAAAGGCCATTTGAAGGCTCCATATGTGGCTCCAGGCTCCCAT 502
QY 709 GG 710
Db      |||
503 GG 504
```

```
RESULT 30
US-11-128-049-2706
; Sequence 2706, Application US/11128049
; Publication No. US20060010513A1
; GENERAL INFORMATION:
; APPLICANT: Melville, Mark W.
; APPLICANT: Charlebois, Timothy S.
; APPLICANT: Mounts, William M.
; APPLICANT: Hann, Louane E.
; APPLICANT: Sinacore, Martin S.
; APPLICANT: Leonard, Mark W.
; APPLICANT: Brown, Eugene L.
; APPLICANT: Miller, Christopher P.
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; PRIOR FILING DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2706
; LENGTH: 505
; TYPE: DNA
; ORGANISM: Cricetus griseus
US-11-128-049-2706

Query Match      14.1%; Score 292.4; DB 16; Length 505;
Best Local Similarity 80.8%; Pred. No. 6.6e-70;
Matches 341; Conservative 0; Mismatches 81; Indels 0; Gaps 0;
```

```
QY 289 CTTTCCACAGAACTTCTGCAATGTCCCATCAACTCTCAGCTGCCTCACTGCAAAAGGA 348
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
83 CTAAGCCGACGACCTGTTACCATGTCCCATCAACTCGAGCTGCCTGACTGAGNAGGG 142
QY 349 GGACAGCCCCAGTGAAGACACAGGAAATGGACCCCCACCTGGCCCCACCCAAACCTGGA 408
Db      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
143 TGACAGCCTCTGTGAGACCCGAGGAAATGAACCCCTTAATAAGGTTTCAACCCAGCCTGGA 202
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QY 409 CACGTTTACCCCGAGGAGCTGCTGCAGCAGATGAAAGAGCTCCTGACCAGAACCA 468  
|||  
Db 203 CACATTCACTCCTGAGGAGATGCTGCAGCAAAATGAAGGAACTCCTGCTGTGAGAACCA 262  
|||  
QY 469 GCTGAAGAAGCCATGAAGCTTAATATCAAGCCATGAAGGAGATTTGAGGAGCTTTC 528  
|||  
Db 263 GCTGAAGAAGCCATGAAGCTTAATCAATCAAGCCATGAAGGAGATATGAGGAGCTTTC 322  
|||  
QY 529 GGCCTGACAGAGAAAACAGAAAGGAAGAACGCCAGTTTTTTTGGAGATACAGAGCAAGAAC 588  
|||  
Db 323 AGCTGGCAGAGAAAGCAGAGGAGAAACGACAGTTGTTTGACACACAGAACAAAGAAC 382  
|||  
QY 589 AAAAGAGCGTCTAATGCGCTTGAATCATGAGAAATGAGAAATGAGGAAAGAGCTTGGAAA 648  
|||  
Db 383 TAAGAAGCTCCTGATGACCTTGAGTTATGAAATGAGAAATGAGAACTGAAGGTGAGCTTGGAAA 442  
|||  
QY 649 ACTAAAGGGAATCAGAAAGGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAG 708  
|||  
Db 443 ACTAAGAGAGAGTCAAGAAAGCCATTTGAAGGCTCCATATGTGGCTCCAGGCTCCCAT 502  
|||  
QY 709 GG 710  
||  
Db 503 GG 504

## RESULT 31

US-11-128-049-6348  
; Sequence 6348, Application US/11128049  
; Publication No. US20060010513A1  
; GENERAL INFORMATION:  
; APPLICANT: Melville, Mark W.  
; APPLICANT: Charlebois, Timothy S.  
; APPLICANT: Mounts, William M.  
; APPLICANT: Hann, Louane E.  
; APPLICANT: Sinacore, Martin S.  
; APPLICANT: Leonard, Mark W.  
; APPLICANT: Brown, Eugene L.  
; APPLICANT: Miller, Christopher P.  
; TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
; FILE REFERENCE: 01997.027700  
; CURRENT APPLICATION NUMBER: US/11/128,049  
; PRIOR FILING DATE: 2005-05-11  
; PRIOR APPLICATION NUMBER: US 60/570,425  
; NUMBER OF SEQ ID NOS: 7285  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 6348  
; LENGTH: 505  
; TYPE: DNA  
; ORGANISM: Cricetulus griseus  
US-11-128-049-6348

Query Match 14.1%; Score 292.4; DB 16; Length 505;  
Best Local Similarity 80.8%; Pred. No. 6.6e-70;  
Matches 341; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY 289 CTTTTCACAGGAACCTCTGCAATGTCCTCCATGCTCCATCAACCTCTCAGCTGCTCACTGAAAGGA 348  
|||  
Db 83 CTAAGCCGACGGACCTGTTTACCATGTCCCATCAACCTCCGAGCTGCTGACTGAGAAGGG 142  
|||  
QY 349 GGACAGCCCGAGTGAAGACAGAGAAATGGACCCCGCCACCTGCGCCACCAACCTGGA 408  
|||  
Db 143 TGACAGCTCTGTGAGACCCAGGAATGAAACCCCTTAATAGTTTCAACCCAGCTTGG 202  
|||  
QY 409 CACGTTTACCCCGAGGAGCTGCTGCAGCAGATGAAAGAGCTCCTGACCAAGAACCA 468  
|||  
Db 203 CACATTCACTCCTGAGGAGATGCTGCAGCAAAATGAAGGAACTCCTGTTGAGAACCA 262  
|||  
QY 469 GCTGAAGAAGCCATGAAGCTTAATATCAAGCCATGAAGGAGATTTGAGGAGCTTTC 528  
|||  
Db 263 GCTGAAGAAGCCATGAAGCTTAACCAATCAAGCCATGAAGGAGATGAGGAGCTTTC 322  
|||

QY 529 GGCTGACAGAGAAAACAGAAAGGAAGAACGCCAGTTTTTTTGGAGATACAGAGCAAGAAC 588  
|||  
Db 323 AGCTGGCAGAGAAAGCAGAGGAGAAACGACAGTTGTTTGACACACAGAACAAAGAAC 382  
|||  
QY 589 AAAAGAGCGTCTAATGCGCTTGAATCATGAGAAATGAGAAATGAGGAAAGAGCTTGGAAA 648  
|||  
Db 383 TAAGAAGCTCCTGATGACCTTGAGTTATGAAATGAGAAATGAGAACTGAAGGTGAGCTTGGAAA 442  
|||  
QY 649 ACTAAAGGGAATCAGAAAGGTCATCTGAGGACCCCACTGATGACTCCAGGCTTCCAG 708  
|||  
Db 443 ACTAAGAGAGAGTCAAGAAAGCCATTTGAAGGCTCCATATGTGGCTCCAGGCTCCCAT 502  
|||  
QY 709 GG 710  
||  
Db 503 GG 504

## RESULT 32

US-09-960-352-11994  
; Sequence 11994, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 11994  
; LENGTH: 396  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; OTHER INFORMATION: Clone ID: 51-LIB34-028-Q1-E1-E4  
US-09-960-352-11994

Query Match 11.5%; Score 238.2; DB 3; Length 396;  
Best Local Similarity 77.7%; Pred. No. 6.3e-55;  
Matches 321; Conservative 0; Mismatches 73; Indels 19; Gaps 2;

QY 737 CTCAGGACCCAGGTGTGAGGCTACAAGCAGAGAAAGCAGACCTGTTGGGCATCGTGCT 796  
|||  
Db 1 CTGAAGACAAAGGTGGCAGCGCTCCAGCTGAAAGAGCAGATCTGCTGGGCATCGTGCT 60  
|||  
QY 797 GAACTGCAGCTCAAGCTGAACTCCAGCGGCTCCTCAGAGACTCCTTTGTTGAAATPAGG 856  
|||  
Db 61 GAATTGCAACTCAAGCTGAACTCAAGCGGCTCCTCCGAGACTCCTTTGTTGAAATCAGG 120  
|||  
QY 857 ATGGCTGAAGGAGAACAGAGGTCAGTAAAGAAATCAAGCATAGTCTCTGGGCCACG 916  
|||  
Db 121 ATGGGTGAAGGGGAAGCAGCTGTGGGAGCACAGAAATCAAGCAGATCTCTGGGCCAC 180  
|||  
QY 917 AGAACAGTCTCCACTGCGACGGCATTTGTCTAAATATAGGAGCAGATCTGCAGATGGG 976  
|||  
Db 181 AGAACTGATTCTCCGTTGACAC-----GAGCAATCTGCAGAGGTACC 222  
|||  
QY 977 AGAATTAATCTCGAATCAGGAGTTAACTGTGAGCCAGCTCCTGCTGTGCTTAAGGAA 1036  
|||  
Db 223 AGGAATTAATGTGGAGTTTGGGAAATTAATCTGTGAGCCAGCTCTGCTGATTTGCCAAG 282  
|||  
QY 1037 GGAATCAGAGGTGAGAGACTTGAAGTTGCACTCAAGGAGGCCAAAGAAAGATTCA 1096  
|||  
Db 283 TGAACACAGAGGTGAGAGACTTGAAGTTGCTTCAAGGAGCCAAAGAAAGAAATTTCT 342  
|||  
QY 1097 GATTTTGAAGAAAGAAAGTAACTCTGAGA-TTGAACCCACAGACAGG 1148  
|||  
Db 343 GATTTTGAAGAAAGAAAGCCAGGATCATTCGAGACCGGAGACCACAGACAGG 395  
|||

```
RESULT 33
US-10-956-157-10262
; Sequence 10262, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10262
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-10262

Query Match          10.4%; Score 216; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.2e-48;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1862 CAGAGTCGTGTCATGGGCGGAGAACAGTGAAGTCTGACCCAGCGCTTACCTTGTTCAAAGA 1921
DB 1 CAGAGTCGTGTCATGGGCGGAGAACAGTGAAGTCTGACCCAGCGCTTACCTTGTTCAAAGA 60

QY 1922 GGAGCTGAGCAGCAGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCCCAAG 1981
DB 61 CGAGCTGAGCAGCAGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCCCAAG 120

QY 1982 TCTGGAGAGTTCTGCTACATAGACAGCTTACAGATTACGTCATGATGATTCATTCATT 2041
DB 121 TGTGGAGAGTTCTGCTGACATAGACAGCTTACAGATTACGTCATGATGATTCATTCATT 180

QY 2042 TAAAGTGTGATGATATCACCTCCCAAACTGTTGGT 2077
DB 181 TAAAGTGTGATGATATCACCTCCCAAACTGTTGGT 216

RESULT 34
US-10-627-757-3
; Sequence 3, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 1203
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-3

Query Match          9.9%; Score 206; DB 8; Length 1203;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 AGAAGCCATGAAGCTAAATAATCAAGCCATGAAGGAGATTGAGGAGCTTTGGGCGCTG 534
DB 499 AGAAGCCATGAAGCTAAATAATCAAGCCATGAAGGAGATTGAGGAGCTTTGGGCGCTG 558

QY 535 GACAGAAACAGAGAGAGAGCGCAGTGTGATGATACAGAGAAAGAGCAAAAGA 594
DB 535 GACAGAAACAGAGAGAGAGCGCAGTGTGATGATACAGAGAAAGAGCAAAAGA 594
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Db 559 GACAGAGAAACAGAGAGAGAGCGCAGTGTGATGATACAGAGAAAGAGCAAAAGA 618
QY 595 GCGTCTAATGCGCTTGAGTCATGAGTAATGAGAAATTTGAGGAGAGCTTTGGAAACTAAA 654
DB 619 GCGTCTAATGCGCTTGAGTCATGAGTAATGAGAAATTTGAGGAGAGCTTTGGAAACTAAA 678
QY 655 AGGAAATCAGAAAGGTCTATCTGAGG 680
DB 679 AGGAAATCAGAAAGGTCTATCTGAGG 704

RESULT 35
US-10-091-281-2
; Sequence 2, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 46951
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: allele
; LOCATION: 391
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 691
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 709
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 887
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 894
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 987
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 1112
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 1505
; OTHER INFORMATION: insertion of additional c residue
; NAME/KEY: allele
; LOCATION: 1606
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 2405
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 2606
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 3313
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
; LOCATION: 3555
; OTHER INFORMATION: insertion of additional t residue
; NAME/KEY: allele
; LOCATION: 3625
; OTHER INFORMATION: single nucleotide polymorphism (SNP)
; NAME/KEY: allele
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LOCATION: 3629  
; OTHER INFORMATION: single nucleotide polymorphism (SNP)  
; NAME/KEY: allele  
LOCATION: 3882  
; OTHER INFORMATION: insertion of additional t residue  
; NAME/KEY: allele  
LOCATION: 3988  
; OTHER INFORMATION: single nucleotide polymorphism (SNP)  
; NAME/KEY: allele  
LOCATION: 4452  
; OTHER INFORMATION: single nucleotide polymorphism (SNP)  
; NAME/KEY: repeat region  
LOCATION: 598..878  
; OTHER INFORMATION: repeat element  
; NAME/KEY: repeat region  
LOCATION: 938..957  
; OTHER INFORMATION: Short repeat element  
; NAME/KEY: repeat region  
LOCATION: 1002..1329  
; OTHER INFORMATION: ALU repeat element  
; NAME/KEY: repeat region  
LOCATION: 2288..2587  
; OTHER INFORMATION: ALU repeat element  
; NAME/KEY: misc\_feature  
LOCATION: 5054  
; OTHER INFORMATION: putative transcription start site  
US-10-091-281-2

Query Match 9.9%; Score 206; DB 7; Length 46951;  
Best Local Similarity 100.0%; Pred. No. 7.9e-45;  
Matches 206; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 475 AGAAGCCATGAAGTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTTCGGCCTG 534  
Db 15116 AGRAGCCATGAAGTAAATAATCAAGCCATGAAGGAGATTTGAGGAGCTTTTCGGCCTG 15175  
QY 535 GACAGAGAAACAGAGAGAGAACGCCAGTCTTTTGTAGATACAGAGCAAGAGAAAGCAAAAGA 594  
Db 15176 GACAGAGAAACAGAGAGAGAACGCCAGTCTTTTGTAGATACAGAGCAAGAGAAAGCAAAAGA 15235  
QY 595 GCGTCTAATGGCTTGAGTCATGAGATGAGAAATTTGAAGGAAGAGCTTGGAAAACTAAA 654  
Db 15236 GCGTCTAATGGCTTGAGTCATGAGATGAGAAATTTGAAGGAAGAGCTTGGAAAACTAAA 15295  
QY 655 AGGGAATCAGAAAGTCTATCTGAGG 680  
Db 15296 AGGGAATCAGAAAGTCTATCTGAGG 15321

RESULT 36  
US-09-960-352-7573  
; Sequence 7573, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; FILE REFERENCE: 16511.006/37-21 (10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 7573  
; LENGTH: 283  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: unsure  
LOCATION: (32), (218)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 33-BOVMS1-004-Q1-E1-A2

US-09-960-352-7573  
Query Match 9.8%; Score 202.6; DB 3; Length 283;  
Best Local Similarity 82.0%; Pred. No. 3.9e-45;  
Matches 232; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
QY 1107 AGAAAAACAAGTAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAGAAAGAGA 1166  
Db 1 AGAAAGCCCAAGGATCATTTCTGAGACTGAGACNCAGACAGAGGAGCAGACAGAAACAAGAGA 60  
QY 1167 ATGATCAAGAGAAAGCCCGGAGACTGTTGGAAGCGAAGTGGAGGACACTCAACCTCCAGG 1226  
Db 61 AGAAGAGGAGAGAAAGACACCAAAACATTTGGAAGTGAAGTGGAAACACTGAAACCTTCAGG 120  
QY 1227 TGACATCTCTGTTTAAAGGAGCTTTCAAGAGGCTCATACAAACTCAGCGAAGCTGAGCTAA 1286  
Db 121 TGACAAACCTGTTTAAAGGAGCTTTCAAGAGGCTCACACGAAACTCAGTGAAGCTGAGCTAA 180  
QY 1287 TGAAGAGAGACTTTCAAGAAAAGTGTACGCCCTTGAAGGAAAAATTTCTGCAATTCAT 1346  
Db 181 TGAAGAGAGACTTTCAAGAAAATGTACGCCCTTGANAGGAAAAATTCGCAAAACCAA 240  
QY 1347 CAGAGTTGAATGAAGAGCAGAGCTTGTATTATCTAACAAAA 1389  
Db 241 CAAACTGAATGAAAAACAGAACTGGGTTTATAATAAAACAAAA 283

RESULT 37  
US-09-918-995-6208  
; Sequence 6208, Application US/09918995  
; Publication No. US20030073623A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc.  
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES  
; FILE REFERENCE: 20411-756  
; CURRENT APPLICATION NUMBER: US/09/918,995  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: US/09/235,076  
; PRIOR FILING DATE: 1999-01-20  
; NUMBER OF SEQ ID NOS: 38054  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6208  
; LENGTH: 380  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-918-995-6208

Query Match 9.5%; Score 198; DB 3; Length 380;  
Best Local Similarity 100.0%; Pred. No. 8.8e-44;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1880 AGAAACAAGTGACTCTGACCAGCAGGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGAC 1939  
Db 1 AGAAACAAGTGACTCTGACCAGCAGGCTTACCTTGTTCAAAGAGGAGCTGAGGACAGGAC 60  
QY 1940 TGGCGGCAACAGCGGAATATTCGATTCTCTGCCCAAGTGTGAGAGGTTCTGCCT 1999  
Db 61 TGGCGGCAACAGCGGAATATTCGATTCTCTGCCCAAGTGTGAGAGGTTCTGCCT 120  
QY 2000 GACATAGACACGTTACAGATTACGTTGATGATTCATTTAAGTGTGATGATCAC 2059  
Db 121 GACATAGACACGTTACAGATTACGTTGATGATTCATTTAAGTGTGATGATCAC 180  
QY 2060 CTCCCCAAAACTGTTGGT 2077  
Db 181 CTCCCCAAAACTGTTGGT 198  
RESULT 38  
US-10-956-157-7613  
; Sequence 7613, Application US/10956157  
; Publication No. US20050118625A1

```
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956,157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7613
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-7613

Query Match          9.3%; Score 194; DB 10; Length 600;
Best Local Similarity 100.0%; Pred. No. 1.5e-42;
Matches 194; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1884 CAAAGTACTCTGACGACGAGCTTACCTGTGTTCAAGAGGAGCTGAGGACAGGGACTGCG 1943
DB 1 CAAAGTACTCTGACGACGAGCTTACCTGTGTTCAAGAGGAGCTGAGGACAGGGACTGCG 60

QY 1944 GCGAACAGCGGAATATTCGATTTCCTCTGCCCCAAGTGTGGAGAGGTTCTGCTTGACA 2003
DB 61 GCGAACAGCGGAATATTCGATTTCCTCTGCCCCAAGTGTGGAGAGGTTCTGCTTGACA 120

QY 2004 TAGACACGTTACAGATTACGTTACGTTGAGTGTGATGATCATATTAAAGTGTGATGATCATCCTCC 2063
DB 121 TAGACACGTTACAGATTACGTTGAGTGTGATGATCATATTAAAGTGTGATGATCATCCTCC 180

QY 2064 CCAAAACTGTTGGT 2077
DB 181 CCAAAACTGTTGGT 194

RESULT 39
US-10-627-757-2
; Sequence 2, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1166
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-2

Query Match          9.2%; Score 190.4; DB 8; Length 1166;
Best Local Similarity 99.5%; Pred. No. 2.1e-41;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 285 GTGACTTTCCACAGGAATCTTGCATGCTCCATCAACTCTCAGTGCCTCACTGAAA 344
DB 475 GTGACTTTCCACAGGAATCTTGCATGCTCCATCAACTCTCAGTGCCTCACTGAAA 534

QY 345 AGGAGGACAGCCCGCTGAAAGCACAGGAAATGGACCCCGCCACCTGGCCCAACCAACC 404
DB 535 AGGAGGACAGCCCGCTGAAAGCACAGGAAATGGACCCCGCCACCTGGCCCAACCAACC 594

QY 405 TGGACACGTTTACCCCGGAGGAGCTGCTCAGCAGATGAAGAGCTCTGACCAAGAAC 464
DB 405 TGGACACGTTTACCCCGGAGGAGCTGCTCAGCAGATGAAGAGCTCTGACCAAGAAC 464
```

```
DB 595 TGGACACGTTTACCCCGGAGGAGCTGCTCAGCAGATGAAGAGCTCTGACCGAGAAC 654
QY 465 ACCAGCTGAAG 476
DB 655 ACCAGCTGAAG 666

RESULT 40
US-10-627-757-4
; Sequence 4, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1183
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-4

Query Match          9.0%; Score 186; DB 8; Length 1183;
Best Local Similarity 100.0%; Pred. No. 3.6e-40;
Matches 186; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 678 AGGACCCCACTGATGATCTCCAGGCTTCCAGGGCCGAAAGCGAGCAGGAAAGGACCAGC 737
DB 499 AGGACCCCACTGATGATCTCCAGGCTTCCAGGGCCGAAAGCGAGCAGGAAAGGACCAGC 558

QY 738 TCAGGACCCAGGTGTGAGGCTTACAGCAGAGAGGAGACCTGTTGGGCATCTGCTCTG 797
DB 559 TCAGGACCCAGGTGTGAGGCTTACAGCAGAGAGGAGACCTGTTGGGCATCTGCTCTG 618

QY 798 AACTGCAGCTCAAGCTGAACCTCCAGCGGCTCCTCAGAAGATTCTTTGTTGAAATTAGGA 857
DB 619 AACTGCAGCTCAAGCTGAACCTCCAGCGGCTCCTCAGAAGATTCTTTGTTGAAATTAGGA 678

QY 858 TGGCTG 863
DB 679 TGGCTG 684

RESULT 41
US-10-627-757-11
; Sequence 11, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-11

Query Match          7.8%; Score 162.4; DB 8; Length 1159;
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-6

Query Match      7.5%; Score 155.8; DB 8; Length 1153;
Best Local Similarity 88.5%; Pred. No. 8.4e-32;
Matches 169; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 934 CACGGCATTGCTTAAATATAGGAGCAGATCTGCAGATGGGGCCCAAGAATTACTTCAACA 993
    |||
Db 498 CAGGGCATTGCTTAAATATAGGAGCAGATCTGCAGATGGGGCCCAAGAATTACTTCAACA 557

QY 994 TGAGGAGTTAACTGTGAGCCAGCTCTCTGTGTCCTTAAGGAGGAAATCAGAAGGTGGA 1053
    |||
Db 558 TGAGGAGTTAACTGTGAGCCAGCTCTCTGTGTCCTTAAGGAGGAAATCAGAAGGTGGA 617

QY 1054 GAGACTTGAAGTTGCACTCAAGGAGGCCCAAGAAAGAGTTTCAGATTTTGAAGAAAC 1113
    |||
Db 618 GAGACTTGAAGTTGCACTCAAGGAGGCCCAAGAAAGAGTTATGAAATAGGTTAACTTGAAT 677

QY 1114 AAGTAATCGTT 1124
    |||
Db 678 ATGTGTTTTTT 688

RESULT 44
US-10-627-757-9
; Sequence 9, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 1150
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-9

Query Match      7.3%; Score 152.4; DB 8; Length 1150;
Best Local Similarity 99.4%; Pred. No. 7.3e-31;
Matches 153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1307 AAGTGTGAGGCCCTTGAAAGGAAATTTCTGCAATTCATCCATCAGAGTTGAATGAAAGCAA 1366
    |||
Db 499 AGGTGTGAGGCCCTTGAAAGGAAATTTCTGCAATTCATCCATCAGAGTTGAATGAAAGCAA 558

QY 1367 GAGCTTGTGTTTATACTAAACAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATC 1426
    |||
Db 559 GAGCTTGTGTTTATACTAAACAAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATC 618

QY 1427 AAAATGGAACAGGCTTAAACACAGAGGATGAAAGT 1460
    |||
Db 619 AAAATGGAACAGGCTTAAACACAGAGGATGAAAGT 652

RESULT 45
US-10-627-757-12
; Sequence 12, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK

; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-14

Query Match      7.6%; Score 157; DB 8; Length 1122;
Best Local Similarity 100.0%; Pred. No. 3.8e-32;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1921 AGGAGCTGAGCAGAGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA 1980
    |||
Db 499 AGGAGCTGAGCAGAGGACTGGCGGCAACAGCGGAATATTCGATTCATTCCTGCCCCAA 558

QY 1981 GTGTGGAGAGGTTCTGCCTGACATAGACAGTTACAGATTCACGTGATGATTCATCAT 2040
    |||
Db 559 GTGTGGAGAGGTTCTGCCTGACATAGACAGTTACAGATTCACGTGATGATTCATCAT 618

QY 2041 TTAAGTGTGATGTATCACCTCCCAAACTGTTGGT 2077
    |||
Db 619 TTAAGTGTGATGTATCACCTCCCAAACTGTTGGT 655

RESULT 43
US-10-627-757-6
; Sequence 6, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 1153
```



```
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 1131
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-627-757-12

Query Match          6.4%; Score 135.4; DB 8; Length 1131;
Best Local Similarity 99.3%; Pred. No. 3.8e-26;
Matches 136; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1709 CAGATGGAAGTTACTGTTCTGATTTTCATGTTGTAAGAGCGGAGAGAGAAATTCAT 1768
      |||||||
Db 498 CAGATGGAAGTTACTGTTCTGATTTTCATGTTGTAAGAGCGGAGAGAGAAATTCAT 557
      |||||||

QY 1769 GAGGAAAAGGACCACTGCGATTCGAGCTGGCAGTTCTGCTGAAGAGAGATGATGCTTTC 1828
      |||||||
Db 558 GAGGAAAAGGACCACTGCGATTCGAGCTGGCAGTTCTGCTGAAGAGAGATGATGCTTTC 617
      |||||||

QY 1829 GAAGACGGAGCGAGCA 1845
      |||||||
Db 618 GAAGACGGAGCGAGTGA 634
      |||||||

RESULT 46
US-10-750-185-4641
; Sequence 4641, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4641
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT07354
US-10-750-185-4641

Query Match          6.4%; Score 133.2; DB 10; Length 600;
Best Local Similarity 80.4%; Pred. No. 1.1e-25;
Matches 156; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 678 AGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGAGCAAGAAAGGACCAGC 737
      |||||||
Db 362 AGGACATCATTTGGGACCCCAAGTCCCAAGCGGAGAGTGGAAACAAGAGTGAACAGC 421
      |||||||

QY 738 TCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAGGAGAGCTGTTGGGCATCGTGTCTG 797
      |||||||
Db 422 TGAAGACCCAGGTGGTGAGGCTTCAAGCTCCAAAGCTGAAAGGAGAGATCTGCTGGGCATCGTGTCTG 481
      |||||||

QY 798 AACTGCAGCTCAAGCTGAAGTCCAGCGGCTCCTCAGAAGATTCCTTTGTTGAAATTAGGA 857
      |||||||
Db 482 AATTGCAACTCAAGCTGAAGTCCAGCGGCTCCTCAGAAGATTCCTTTGTTGAAATTAGGA 541
      |||||||

QY 858 TGGCTGAAGAGGAA 871
      |||||||
Db 542 TGGCTGTAAGTGTA 555
      |||||||

RESULT 48
US-10-627-757-10
; Sequence 10, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASGO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-10

Query Match          6.4%; Score 133.2; DB 10; Length 600;
Best Local Similarity 80.4%; Pred. No. 1.1e-25;
Matches 156; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 678 AGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGAGCAAGAAAGGACCAGC 737
      |||||||
Db 362 AGGACATCATTTGGGACCCCAAGTCCCAAGCGGAGAGTGGAAACAAGAGTGAACAGC 421
      |||||||

QY 738 TCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAGGAGCAACCTGTTGGGCATCGTGTCTG 797
      |||||||
Db 422 TGAAGACCCAGGTGGGCACGCTCCAAAGCTGAAAGGAGAGATCTGCTGGGCATCGTGTCTG 481
      |||||||

QY 798 AACTGCAGCTCAAGCTGAAGTCCAGCGGCTCCTCAGAAGATTCCTTTGTTGAAATTAGGA 857
      |||||||
Db 482 AATTGCAACTCAAGCTGAAGTCCAGCGGCTCCTCAGAAGATTCCTTTGTTGAAATTAGGA 541
      |||||||

QY 858 TGGCTGAAGAGGAA 871
      |||||||
```

```
Db 542 TGGCTGTAAGTGTA 555
      |||||||

RESULT 47
US-10-750-623-4641
; Sequence 4641, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4641
; LENGTH: 600
; TYPE: DNA
; ORGANISM: Bovine MMBT07354
US-10-750-623-4641

Query Match          6.4%; Score 133.2; DB 10; Length 600;
Best Local Similarity 80.4%; Pred. No. 1.1e-25;
Matches 156; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 678 AGGACCCCACTGATGACTCCAGGCTTCCAGGGCCGGAAGCGGAGCAAGAAAGGACCAGC 737
      |||||||
Db 362 AGGACATCATTTGGGACCCCAAGTCCCAAGCGGAGAGTGGAAACAAGAGTGAACAGC 421
      |||||||

QY 738 TCAGGACCCAGGTGGTGAGGCTACAAGCAGAGAGGAGAGCTGTTGGGCATCGTGTCTG 797
      |||||||
Db 422 TGAAGACCCAGGTGGTGAGGCTTCAAGCTCCAAAGCTGAAAGGAGAGATCTGCTGGGCATCGTGTCTG 481
      |||||||

QY 798 AACTGCAGCTCAAGCTGAAGTCCAGCGGCTCCTCAGAAGATTCCTTTGTTGAAATTAGGA 857
      |||||||
Db 482 AATTGCAACTCAAGCTGAAGTCCAGCGGCTCCTCAGAAGATTCCTTTGTTGAAATTAGGA 541
      |||||||

QY 858 TGGCTGAAGAGGAA 871
      |||||||
Db 542 TGGCTGTAAGTGTA 555
      |||||||

RESULT 48
US-10-627-757-10
; Sequence 10, Application US/10627757
; Publication No. US20040091914A1
; GENERAL INFORMATION:
; APPLICANT: KOUCHI YASUHIRO
; APPLICANT: MASASGO AKINORI
; APPLICANT: TAKAHATI TAKAYUKI
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK
; FILE REFERENCE: Q76319
; CURRENT APPLICATION NUMBER: US/10/627,757
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: JP P2002-226612
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-627-757-10
```

Query Match  
Best Local Similarity 6.0%; Score 124; DB 8; Length 1094;  
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1337 GCAATTCATCAGAGTTGAATGAAGCAAGAGCTTGTATATACAAAAAGTTAGAG 1396  
Db 1 GCAATTCATCAGAGTTGAATGAAGCAAGAGCTTGTATATACAAAAAGTTAGAG 60  
QY 1397 CTACAAGTGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAAAACAGAGGATGAA 1456  
Db 61 CTACAAGTGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAAAACAGAGGATGAA 120  
QY 1457 AAGT 1460  
Db 121 AAGT 124

## RESULT 49

US-09-960-352-14197  
; Sequence 14197, Application US/09960352  
; Patent No. US20020137139A1  
; GENERAL INFORMATION:  
; APPLICANT: Warren, Wesley C.  
; APPLICANT: Tao, Nengbing  
; APPLICANT: Byatt, John C.  
; APPLICANT: Mathialagan, Nagappan  
; TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND  
; TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION  
; FILE REFERENCE: 16511.006/37-21(10298)C  
; CURRENT APPLICATION NUMBER: US/09/960,352  
; CURRENT FILING DATE: 2001-09-24  
; NUMBER OF SEQ ID NOS: 15112  
; SEQ ID NO 14197  
; LENGTH: 170  
; TYPE: DNA  
; ORGANISM: Bos taurus  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (18),(141)  
; OTHER INFORMATION: unsure at all n locations  
; OTHER INFORMATION: Clone ID: 61-BOVMS1-018-Q1-E1-H2  
US-09-960-352-14197

Query Match  
Best Local Similarity 5.8%; Score 120; DB 3; Length 170;  
Matches 145; Conservative 0; Mismatches 22; Indels 3; Gaps 1;  
QY 1727 TCTGATTTTCATGCTGAAGAGCGAGAGAGAGAAATTCATGAGGAAAGGAGCAACTG 1786  
Db 1 TCTGATTTTCATGCTGAAGAGCGAGAGAGAGAGAAATTCATGAGGAAAGGAGCAACTG 60  
QY 1787 GCATTGCGAGTGGCAGTTCTGCTGAAGAGAGATGCTTTTCGAGAGCGAGGAGCAG---G 1843  
Db 61 GCATTGCGAGTGGCAGTTCTGCTGAAGAGAGATGCTTTTCGAGAGCGAGGAGCAG 120  
QY 1844 CAGTCCTTGATGGAGATGAGAGTCGTCATGGGGCGAGAGCAAGTGAATC 1893  
Db 121 CAGACCTTGATGGAAATGCANAGCCGTACGGGGCGAGAGCAAGTGAATC 170

## RESULT 50

US-10-627-757-8  
; Sequence 8, Application US/10627757  
; Publication No. US20040091914A1  
; GENERAL INFORMATION:  
; APPLICANT: KOUCHI YASUHIRO  
; APPLICANT: MASASCO AKINORI  
; APPLICANT: TAKAHATI TAKAYUKI  
; TITLE OF INVENTION: GENE ASSAY METHOD FOR PREDICTING GLAUCOMA ONSET RISK  
; FILE REFERENCE: 076319  
; CURRENT APPLICATION NUMBER: US/10/627,757  
; CURRENT FILING DATE: 2003-07-28  
; PRIOR APPLICATION NUMBER: JP P2002-226612

; PRIOR FILING DATE: 2002-08-02  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 1116  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-627-757-8

Query Match  
Best Local Similarity 5.6%; Score 116.4; DB 8; Length 1116;  
Matches 117; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1193 GTTGGAAAGCGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAA 1252  
Db 501 GTTGGAAAGCGAAGTGAAGCACTGAACCTCCAGGTGACATCTCTGTTTAAAGGAGCTTCAA 560  
QY 1253 GAGGCTCATACAAAACTCAGCGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAAGT 1310  
Db 561 GAGGCTCATACAAAACTCAGCGAAGCTGAGCTTAATGAAGAAGAGACTTCAAGAAAAAGT 618

Search completed: May 30, 2006, 00:41:42  
Job time : 2644 secs

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Db 90 GTTGAAGCAAGCCAGACTGATGAGCCAAAGGAAATCGACTCATACAAATTCAAAAAGA 149  
QY 1555 AGAAAAGTGGACAGGCGAGTGTGAAGGAATCGAGTGAATAAACTGGAACCTGGCAGAGAA 1614  
Db 150 CAAGGAATTCGAAGGAGTTTGAACAAAAGAAATCGCGGTGGTGGTGAATTCGAAGAAGA 209  
QY 1615 GGCTCTGGCTTCAACACAGCTGCAATGATGAATGAAGCAAAACCATTCGCCAAGCAGGA 1674  
Db 210 AGCAGAGGCTGGTGTGCAAGGTGAATTTAGCTGAGNTTAAGAAAAATTCGAGAGAAGAAAA 269  
QY 1675 AGAGGACCTGGAACCATGACCATC 1699  
Db 270 GGATGACGTTGTCAAAAATTTTGATC 294

## RESULT 3

US-11-217-529-190968  
; Sequence 190968, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 190968  
; LENGTH: 507  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-190968

Query Match 2.1%; Score 42.6; DB 7; Length 507;

Best Local Similarity 47.5%; Pred. No. 0.009; Mismatches 139; Indels 0; Gaps 0;

Matches 126; Conservative 0;

QY 1435 ACAGGCTAAACACAGAGGATGAAAGTCCAAATTAAGTGTGCTACAGATGACACACAACAA 1494  
Db 195 ACAAGCTGAAGAAAGGAGCCACGAATAGTATCAAGGCTAGAAAGTACAGACAAGTAA 254  
QY 1495 GCTTCTTCAAGACATAATTAATGCTTGAATAACAAATTTAGGGAATCAACAGAAAAGATC 1554  
Db 255 GTTGAAGCAAGCCAGACTGATGCGCAAGGAAATCGACTCATACAAAAATTCAAAAAGA 314  
QY 1555 AGAAAAGTGGACAGGCGAGTGTGAGGAACTGAGTGAATAAACTGAAATTCGCAAGGAA 1614  
Db 315 CAAGGAATGAAGGAGTTTGAACAAAAGAAATCGCGGTGGTGGTGAATTTGAAAAGAA 374  
QY 1615 GGCTCTGGCTTCCAAACAGCTGCAATGGAATGAAGCAAAACCATTCGCCAAGCAGGA 1674  
Db 375 AGCAGAGGCTGGTGTGCAAGGTGAATTAGCTGAGATTAAGAAAATTCGAGAGAGAAGAA 434  
QY 1675 AGAGGACCTGGAACCATGACCATC 1699  
Db 435 GGATGACGTTGTCAAAAATTTTGATC 459

## RESULT 4

US-11-217-529-6230  
; Sequence 6230, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA

; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6230  
; LENGTH: 990  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-6230

Query Match 2.0%; Score 40.8; DB 7; Length 990;

Best Local Similarity 53.0%; Pred. No. 0.044; Mismatches 87; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

Matches 87; Conservative 0;

QY 1380 CTAACAAAAAGTTAGAGCTACAAAGTGAAGCATGCTATCAGAAATCAAAATCGAACAGG 1439  
Db 332 CTTACAGAGATTCAGAGAGATGAGAAAAAACTGCTTCAGGAACAAAACCAAGAAAGG 391  
QY 1440 CTAACACAGAGGATGAAAAAGTCCAAATTAAGTGTGCTACAGATGACACACAACAGCTTC 1499  
Db 392 CGAAACTAGACGATATAAGCACACCAACATCGATGAAGAGATTCGTAAGAACACAGCAT 451  
QY 1500 TTCAGAACATATATATGCAATTTGAAAAACAATTCAGGAACTAACA 1543  
Db 452 TACAAGAGTTTATGGAACAATGAAGCCCAAGTTTCAACAGTAACA 495

## RESULT 5

US-11-217-529-77435/c  
; Sequence 77435, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 77435  
; LENGTH: 615  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
; NAME/KEY: modified base  
; LOCATION: (152)...(192)  
; OTHER INFORMATION: a, c, g, t, unknown, or other  
US-11-217-529-77435

Query Match 1.9%; Score 40.4; DB 7; Length 615;

Best Local Similarity 40.2%; Pred. No. 0.043; Mismatches 149; Conservative 0; Mismatches 222; Indels 0; Gaps 0;

Matches 149; Conservative 0;

QY 1039 GAATCAGAAAGTGGAGAGACTTGAAGTTGCACTCAAGGAGGCCAAAGAAAGAGTTTCAGA 1098  
Db 458 GAGTTAATAGAAGGATAGTAGTAAGAGAGAAAATAGAGGAAGTAGAGAGAGAGAAAT 399  
QY 1099 TTTTGAAGAAAGAAACAAGTAAATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCACAGA 1158





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; ORGANISM: Saccharomyces pastorianus
US-11-217-529-5260

Query Match
Best Local Similarity 49.1%; Score 39.6; DB 7; Length 2832;
Matches 105; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

QY 1281 AGCTAATGAGAAGAGACTTCAAGAAAGTGTTCAGGCCCTTGAAGAGAAATTTCTCAA 1340
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1325 AGGAATAGACAGAGACTTCGAAACATTTAAACGATGAGGATAGTTACTCGAGTAGCA 1384
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1341 TTCCATCAGAGTTGAATGAAAGCAAGCTTGTATTACTTAACAAAGTTAGAGTAC 1400
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1385 TAGCAAGACCATAGATAAAATTTCTGAAATAGTTGAAATATGAAAGATTTGGACCAAC 1444
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1401 AAGTGGAAAGCATGCTATCGAAATCAAAATGGAACAGGCTTAAACAGAGATGAAAAAGT 1460
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1445 ATGTGGATGAATCCAGTATGCAACGCGCTGAACAAAAATGAAAAAGATGAGTCTG 1504
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1461 CCAATTAATGTGCTACAGATGACACAAACAA 1494
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1505 CCGTATTCAATGAATGAGTGCCCGCAACGA 1538
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
US-11-217-529-79917
; Sequence 79917, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 79917
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-79917

Query Match
Best Local Similarity 1.9%; Score 39.4; DB 7; Length 2007;
Matches 142; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 1248 TTCAGAGGCTCATACAAACTCAGCGAAGCTGAGCTAATGAAGAGAGACTTCAAGAA 1307
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 725 TTAACATAAACATACATCAATAAGAGAACTCTGGAGAACGGTGAGACTCGTATGAAA 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1308 AGTGTGAGGCCCTTGAAGAGAAAATCTGCAATCCATCAGAGTTCAATGAAAGCAAG 1367
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 785 TGTTAATGAATTTGTTAAGAAAACCTTCCGAAGAAATAGACAGTTTGAATGAGGATGTCG 844
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1368 AGCTTGTATTACTAACAAAAGTTAGAGCTACAAAGTGAAGCATGCTATCAGAATCA 1427
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 845 AGGAATCAAACTTCAGAAAGAAAAGAACTACACAAAGAGGCACAACTTCCAAGTTGG 904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1428 AAATGGAACAGGCTTAAACAGAGATGAAAGTCCAAATTAATGTGCTACAGATGACAC 1487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 905 AAAATAAGGAGACGGTCTTTTAAATGAAATTTCTCGTTTGAATACTTCACTGTCGATA 964
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1488 ACAACAGCTTCTTCAAGACATAAATGCAATGAAACAAATTTAGGACTAACAGAA 1547
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 965 AAGTAGAAAATTTGAATGATACTACTGAAAAATCAAAAGGCTCTGGAGTCAAGAAATTCGAA 1024
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-82102

Query Match          1.9%; Score 39; DB 7; Length 1212;
Best Local Similarity 47.4%; Pred. No. 0.16;
Matches 117; Conservative 0; Mismatches 130; Indels 0; Gaps 0;

QY 965 GCAGATGGGGCCCAAGAAATTAACCTCGAACATGAGGAGTAACTGTGAGCCAGCTCCTGCTG 1024
Db 1196 GAAGAGAAAGCCACTGTTTCTTGATGAAGAGGAGGATGCTTTTCGAGTGAACATAATG 1137

QY 1025 TGCCTAAGGGAAGGGAATCAGAAGGTGGAGACTTTGAAGTTGCACTCAAGGAGGCGCAAA 1084
Db 1136 GAACATAGATGTGCTGCTGATGAGGAAGCAAGTGTTTATAGATGAAGTACGCTCGAAGAA 1077

QY 1085 GAAAGAGTTTCAGATTTTGAAGAAGAAAACAAGTAATCGTTCTGAGATTGAAACCCAGACA 1144
Db 1076 GATGGAGATCTGGATGAAGAGGAAGATACAGAAGACGAAGAAGATACAGTGGGAAGAAC 1017

QY 1145 GAGGGGACACAGAGAAAGAGAAATGATGAAGAGAAAGGCCCGGAGACTGTTTGAAGCGAA 1204
Db 1016 GAGGAAGATACAGTGGAAAGACCGCGGAAGAGATACAGTGGAAAGAAACCGGAGGAGATACA 957

QY 1205 GTGGAAG 1211
Db 956 GTGGAAG 950

RESULT 12
US-11-217-529-78674
; Sequence 78674, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 78674
; LENGTH: 2466
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78674

Query Match          1.9%; Score 38.8; DB 7; Length 2466;
Best Local Similarity 45.4%; Pred. No. 0.28;
Matches 139; Conservative 0; Mismatches 167; Indels 0; Gaps 0;

QY 1281 AGCTAATGAAGAAGAGACTTCAAGAAAGTGTGAGCCCTTGAAAGGAAAAATTTGCAAA 1340
Db 1610 AGGTAGTACAGGATAAATTAATTAATAATGAGGAGACGCTAAAACTTAAAGAAGCTGAAA 1669

QY 1341 TTCCATCAGATTGAATGAAGACAGAGCTGTTTATACTACAAAAGATTAGAGCTAC 1400
Db 1670 TTGAATTCATTAATAGTGAATGGAGCTGAAAAAAGCAGATCACTCAAAAAGATGATG 1729

QY 1401 AAGTGGAAAGCAGCTTATCAGAAATCAAAATGAAACAGGCTAAAAACAGAGGATGAAAAAGT 1460
Db 1730 AATTTAAGATGTGGCAAGCAAAATACGAAACTGTGCAAGACGAAGCTAAGATACGCAATG 1789

QY 1461 CCAATTAATCTGCTACAGATGACACACACAGCTTCTTCAAGACATATATATGCAAT 1520
Db 1790 CCGAAGTTACAGAGTTGAACCGGAGATATTGAAGATCTAAAGGAATCAAAATTTGCAATTTGG 1849
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QY 1521 TGAAAAACAATTGAGGAACCTAAACAAGAAAGAGTCAGAAAAAGTGACAGGCGAGTCTGCA 1580
Db 1850 AAGAAACAATTACGGAACCTAGAAAACAAGTTCATAAACTAGAAAAATGAGTGTGAACGG 1909

QY 1581 AGGAAC 1586
Db 1910 AGAAAC 1915

RESULT 13
US-11-217-529-174162/c
; Sequence 174162, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 174162
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-174162

Query Match          1.8%; Score 38.2; DB 7; Length 768;
Best Local Similarity 46.7%; Pred. No. 0.21;
Matches 121; Conservative 0; Mismatches 138; Indels 0; Gaps 0;

QY 965 GCAGATGGGGCCCAAGAAATTAACCTCGAACATGAGGAGTAACTGTGAGCCAGCTCCTGCTG 1024
Db 422 GAAGAGGAAGCCACTGTTTCTTGATGAAGAGGAGGATTCGTTTTCGAGTGAACATAATG 363

QY 1025 TGCCTAAGGGAAGGGAATCAGAAGGTGGAGAGACTTTGAAGTTGCACTCAAGGAGGCGCAAA 1084
Db 362 GAACATAGATGTGTTGGCTGATGAGGAACAAGTGTTTTAGATGAAGTAGCGGTCCAAGAA 303

QY 1085 GAAAGAGTTTCAGATTTTGAAGAAAGAAAACAAGTAATCGTTCTGAGATTGAAACCCAGACA 1144
Db 302 GATGGAGATGTGGATGAAGAGGAAGATACAGAAGACGAAGAAGATACAGTGGGAAGAAC 243

QY 1145 GAGGGGACACAGAGAAAGAGAAATGATCAAGAGAAAGGCCCGGAGACTGTTTGAAGCGAA 1204
Db 242 GAGGAAGACACAGTGGAAAGACACCGTGGAAAGACCGCGGAGGAAGATACATAGTAGAAGGAT 183

QY 1205 GTGGAAGCACTGAACCTCC 1223
Db 182 GTAGAGCTGCTGGAATAAC 164

RESULT 14
US-10-953-349-17644/c
; Sequence 17644, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: Patentin version 3.3
```

; SEQ ID NO 17644  
; LENGTH: 1285  
; TYPE: DNA  
; ORGANISM: Glycine max  
US-10-953-349-17644

Query Match  
Best Local Similarity 51.5%; Score 38.2; DB 6; Length 1285;  
Matches 88; Conservative 0; Mismatches 83; Indels 0; Gaps 0;  
  
QY 1253 GAGGCTCATCAAACTCAGCGAGCTGAGCTAATGAAGAGAGACTTCAAGAAAGTGT 1312  
DB 1103 GAGCACAACAATGTCTTTTCAGCTAAGCCAGGTACCATCAACTTTGAATGGAAT 1044  
  
QY 1313 CAGGCCCTTGAAGAGAAAAATTTCTGCAATTCATCAGAGTTGAATGAAAGCAAGAGCTT 1372  
DB 1043 GCAGCATCTTCTGACAACCTTCTCTCAGTTCCATGTGAATCAGATGAAGAGCTAGAGCAT 984  
  
QY 1373 GTTTATCTAACAAGATTAGAGCTACAAGTGAAGATGCTATCAGAA 1423  
DB 983 CTTCCCAACAATACCTCTGTCAACCCCAAGTAGATTGAATTTCTATGAAA 933

## RESULT 15

US-11-217-529-81089  
; Sequence 81089, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 2004-09-02  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 81089  
; LENGTH: 2796  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-81089

Query Match  
Best Local Similarity 44.6%; Score 38; DB 7; Length 2796;  
Matches 149; Conservative 0; Mismatches 185; Indels 0; Gaps 0;  
  
QY 1096 AGATTTTGAAGAGAAACAGTATCGTTCTGAGATTGAACCCAGACAGAGGGGAGCAC 1155  
DB 960 AGAACTAGAGAGAGAGAAAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1019  
  
QY 1156 AGAGAAAGAGATGATGAAGAGAAAGCCCGGAGACTGTTGGAAGCGAGTGAAGCACT 1215  
DB 1020 AGAAAG 1079  
  
QY 1216 GAACCTCCAGTGACATCTCTGTTTAAAGAGCTTCAAGAGGCTCATACAAACTCAGCGA 1275  
DB 1080 AAGGGAAG 1139  
  
QY 1276 AGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGTGTCAAGCCCTTGAAGAGAAAATTC 1335  
DB 1140 AGAGGCTCAAGGAG 1199  
  
QY 1336 TGCAATTTCCATCAGAGTTGAATGAAAGCAAGAGCTGTTTATCTACTAACAAGATTAGA 1395  
DB 1200 TAGATTGGAAG 1259  
  
QY 1396 GCTACAAGTGGAAAGCATGCTATCAGAAATCAAA 1429

DB 1260 GGAACCTAAAACGCAAGAGGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1293

## RESULT 16

US-10-953-349-26062  
; Sequence 26062, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 26062  
; LENGTH: 883  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-10-953-349-26062

Query Match  
Best Local Similarity 48.4%; Score 37.8; DB 6; Length 883;  
Matches 105; Conservative 0; Mismatches 112; Indels 0; Gaps 0;  
  
QY 1044 AGAAGGTGGAGAGACTTGAAGTTGCACTCAAGGAGGCCAAAGAAAGAGTTTCAGATT 1103  
DB 558 AGAACCTTGATGTGATGAAAGCTGCTATTGATGGCTTGCAACACACAGAGGATGATGACG 617  
  
QY 1104 AAAAGAAAAAAGTATCGTTCTGAGATTGAAACCCAGACAGAGGGGAGCAGAGAGAAAG 1163  
DB 618 GCAAGAGAGATGGTGACACATCTGTGAAGAAAAGCAAGAGAGAGAGAGAGAGAGAG 677  
  
QY 1164 AGAATGATCAAGAGAAAGCCCGGAGACTGTTTGAAGCGAAGTGGAGCACTGAACTCC 1223  
DB 678 CTAACGGTGACGCGATGGAGCTTGAGATGCTGCAACAGAGAGCTGAACTGGAAACCGAGA 737  
  
QY 1224 AGGTGACATCTCTGTTTAAAGGAGCTTCAAGAGCTCA 1260  
DB 738 AGAAGAAAGAAAGAAAGCAAGCTTTGAGGAGCCGCA 774

## RESULT 17

US-11-217-529-326  
; Sequence 326, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; PRIOR FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 326  
; LENGTH: 1614  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-326

Query Match  
Best Local Similarity 48.0%; Score 37.2; DB 7; Length 1614;  
Matches 142; Conservative 0; Mismatches 148; Indels 6; Gaps 1;



Db 1775 CAGGAACAGGAGAGAGATGTGGGACGAGGAGGAGAGATGTGTGACGAGGAGAGAG 1834  
Qy 545 CAGAAGGAAGAACCCAGTGTGAGATACAGAGCAAGAGCAAGCAAGAGCGTCTAATG 604  
Db 1835 ATCAAGACAGGAGGAGAGATCGGAGGAGGAGGAGAGATGTGGGAGCAGGAAGT 1894  
Qy 605 GCCTTGAGTCATGAGATGAGAAATGAAAGGAGAGCTTGGAAACTAAAG 656  
Db 1895 AGGCTGGCAGCAGGAGGAGAGATGACGAGAACACGAGGAGCACCTGGAG 1946

## RESULT 21

US-11-217-529-173387  
; Sequence 173387, Application US/11217529  
; Publication No. US20060099612A1  
; GENERAL INFORMATION:  
; APPLICANT: SUNTORY LIMITED  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: S-38-285  
; CURRENT APPLICATION NUMBER: US/11/217,529  
; CURRENT FILING DATE: 2005-09-02  
; PRIOR APPLICATION NUMBER: US 10/932,182  
; PRIOR FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 173387  
; LENGTH: 849  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-11-217-529-173387

Query Match 1.8%; Score 36.6; DB 7; Length 849;  
Best Local Similarity 49.8%; Pred. No. 0.62;  
Matches 120; Conservative 0; Mismatches 119; Indels 2; Gaps 1;  
Qy 1503 AAGAACATAATATGATGAAACATTTAGGAACCTAACAGAAAGATGCTGAGAAAAG 1562  
Db 390 AGGAACGAGAAATCGTCGGAAGACAAAGAAAGAACCGACTATAGAGAAAATAAGAGAAA 449  
Qy 1563 TGCACAGGGCAGTGTGAGGAACTGAGTGAATAA--ACTGGAACCTGCAGAGAGGCTCT 1620  
Db 450 AGAAGAGGACGTCGTAAAGCAAGAAAGCAAGAAAGTAAAGGAATTTGAAACAGCAGTCGGA 509  
Qy 1621 GGCTTCCAAACAGCTGCAATGGATGAAATGAAAGCAAAACCATTTGCCAAGCAGGAAGGGA 1680  
Db 510 GAAGGATAAGAAAGCAAGTTGAAATCTGTTAATAAAAGCATACTAACGATGAGAGGA 569  
Qy 1681 CCTGGAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTCTGATTTTCATGC 1740  
Db 570 GATCGAAAAGATGCCAAATCAAAGGCTGAATTTGGAGCTTTTAATGATGATGATGA 629  
Qy 1741 T 1741  
Db 630 T 630

## RESULT 22

US-10-953-349-3230  
; Sequence 3230, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 3230  
; LENGTH: 908  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-3230

Query Match 1.8%; Score 36.6; DB 6; Length 908;  
Best Local Similarity 49.2%; Pred. No. 0.65;  
Matches 96; Conservative 0; Mismatches 99; Indels 0; Gaps 0;  
Qy 467 CAGCTGAAGAGCCATGAAGCTAAATATCAAGCCATGAAGGGAGATTGAGGAGCTT 526  
Db 540 CCGAGGAAAGGTGCTAGTGTGGAAGTGTCTTGAAGAGAGAGCCAGGCTAGAAGATCTG 599  
Qy 527 TCGGCTTGGACAGAGAAACAGAAAGGAGAGCCAGTCTTTTGGATACAGAGCAAGAA 586  
Db 600 AAGAAGCAGAGAGAGATTGCTGCAGCTGCCGAAAGAGGATGATAAGAAAAAGAGAGAA 659  
Qy 587 GCAAAAGAGCGTCTAATGGCTTTGAGTCTATGAGAAATGAGAGGAAGAGCTTGGGA 646  
Db 660 GCAAAAGCTCTGCAGCTGCTAGATTCAAGCTAAGCTAGACGCTAAGAAAGGTCCAGGC 719  
Qy 647 AAACCTAAAGGGAAA 661  
Db 720 AAAGGAAAGGCCAA 734

## RESULT 23

US-10-953-349-5081  
; Sequence 5081, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 5081  
; LENGTH: 670  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-5081

Query Match 1.8%; Score 36.4; DB 6; Length 670;  
Best Local Similarity 46.5%; Pred. No. 0.61;  
Matches 118; Conservative 0; Mismatches 136; Indels 0; Gaps 0;  
Qy 1125 CTGAGATTGAACCCACAGACAGAGGGGAGCACAGAGAAAGAAATGATGAGAGAAAGGCC 1184  
Db 129 CTGAGAAAGCTGAGAAAGAGGAGAGAAAGGATTAAGATAGGAGGATTAAGAACGAGG 188  
Qy 1185 CGGAGACTTTGGAAGCGAAGTGGGAAGCACTGAACTCCAGGTCACATCTCTGTTTAAGG 1244  
Db 189 ACGATAAAATGTTGGAGGAGAGAAAGGGGAAAGATCAAGAGAGAGCAAGAGAAAG 248  
Qy 1245 AGCTTCAAGAGGCTCATACAAAACCTCAGCGAAGCTCAGCTAATGAAGAGAGACTTCAAG 1304  
Db 249 ATAAGAAAGCGAAGAAAGAGAAAGAACCCCTGAAGATGAAGAAAGATCCAGAGAAAGTGAAGA 308  
Qy 1305 AAAAGTGTCCAGGCCCTTGAAGGAAAAAATTTCTGCAATTCCTCAGATTTGAATGAAAAAGC 1364  
Db 309 TGAAGCTTCAGAAAGATTGAAGAAAAAGATTCAAGCTATGCTTTTAAAGAAAGATGAGATTG 368  
Qy 1365 AAGAGCTTTGTTAT 1378  
Db 369 TGAAGCTTATTCAT 382

RESULT 24

```

US-11-217-529-3877
; Sequence 3877, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3877
; LENGTH: 810
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3877

```

Query Match	1.7%	Score 36.2;	DB 7;	Length 810;
Best Local Similarity	46.9%;	Pred. No. 0.78;		
Matches 113;	Conservative 0;	Mismatches 128;	Indels 0;	Gaps 0;
Qy 1385	AAAAGTTAGAGCTACAAGTGGAAAGCATGCTATCAGAAATCAAAATGGAAACAGGCTAAA	1444		
Db 148	AGAAAGAAGAAATGGACAAGTGGACTGTGGGAAAGCAGAGAACCCTATTTGAAAGTGGTGAA	207		
Qy 1445	ACAGAGATGAAAGTCCAAATTTAACTGTGCTACAGATGACACACACAAGCTTCTTCAA	1504		
Db 208	ACAGAGAATACCTGTATGATATATTTCTTAATTTCAAGACCGTCATCGGAAAAATCAGAAA	267		
Qy 1505	GAACATAATATGCTTTGAAAACAATTTGAGGAACATAACAAGAAAGAGTCAGAAAAAGTG	1564		
Db 268	GAATTTAATGAACACTGGAAAAATGTATGTTGATATCTAAAAACAAGAGAAATTTGTT	327		
Qy 1565	GACAGGCGAGTGTGAAAGGAATCAGTGTGAAAAACTGGAACTGGCAGAGAAGGCTCTGGCT	1624		
Db 328	TGGTTGCGGTGGACTTTGAAATGGACAAAGAAGGTCGTCTGCAATCGAAGGATGCTACT	387		
Qy 1625	T 1625			
Db 388	T 388			

RESULT 25

```

US-11-217-529-1760
: Sequence 1760, Application US/11217529
: Publication No. US20060099612A1
: GENERAL INFORMATION:
: APPLICANT: SUNTORY LIMITED
: APPLICANT: NAKAO, YOSHIHIRO
: APPLICANT: NAKAMURA, NORIHIISA
: APPLICANT: KODAMA, YUKIKO
: APPLICANT: FUJIMURA, TOMOKO
: APPLICANT: ASHIKARI, TOSHIKO
: TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
: FILE REFERENCE: S-38-285
: CURRENT APPLICATION NUMBER: US/11/217,529
: PRIOR FILING DATE: 2005-09-02
: PRIOR APPLICATION NUMBER: US 10/932,182
: PRIOR FILING DATE: 2004-09-02
: NUMBER OF SEQ ID NOS: 197023
: SOFTWARE: PatentIn version 3.3
: SEQ ID NO 1760
: LENGTH: 1446
: TYPE: DNA
: ORGANISM: Saccharomyces pastorianus

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US-11-217-529-1760

```

Query Match      1.7%; Score 36.2; DB 7; Length 1446;
Best Local Similarity 50.3%; Pred. No. 1.1;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

Qy      1501  TCAAGACATAATAATGTCATTGAAAAACAATTGAGGAACCTAACAGAAAAAGAGTCAGAAAA 1560
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1215  TGAAGAGAAGCTAAGCCTTTTGATCAAGGAGAGTTGAACCTTAAGAGAGGAAGTAAGGA 1274

Qy      1561  AGTGGACAGGCGAGTGTCTGAAGGAACCTGAGTGAAAAAACTGGAACTGCGAGAGAAGGCTCT 1620
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1275  AGAGGTTAAGGAAGAGAGAAGGAAGGAAAAAGAGGAGGAAGAGGAAAAAGAGGAAGAAGGA 1334

Qy      1621  GGCTTCCAAACAGCTGCAAAATGGATGAAATGAAGCAAAACATTTCGCCAAGCAGGGAAGA 1677
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      1335  AAAGAAGGAGNAGNAGGAGNAGNAGNATAGNAGGAGNAGNAGGAGNAGNAGAGAAA 1391

RESULT 26
US-10-953-349-5386
; Sequence 5386, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLY
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5386
; LENGTH: 2730
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-953-349-5386

```

Query Match	1.7%; Score 36.2; DB 6; Length 2730;
Best Local Similarity	43.3%; Fred. No. 1.6;
Matches	170; Conservative 0; Mismatches 223; Indels 0; Gaps 0;
QY	1497 TTCCTTCAAGAACATAATAATGCTATTGAAACCAATTGAGGAACCTAACCAAGAAAAGAGTCCAG 1556
Db	580 TACAACATGAAGCTGCACAAGACCAATTCGAACAAAGATGCCAATACAGGACACATCAAG 639
QY	1557 AAAAAGTGGACAGGGCAGTGCTGAAGGAACCTGAGTGAAAACTGGAACTGGCAGAGAAAG 1616
Db	640 AGGAAGGGACACTGCTAGATGAACACAAGGACAGCATATGGATGAAAAAGTTGGAGAATG 699
QY	1617 CTCTGGCTTCCNAACACGCTCCAAATGATGAAATGAAGCAACCACTTCCCAAGCAGGAAG 1676
Db	700 GGGATGAAATATAAACAAAGTGGAGAAATGTTGAAGGAAAGAAAGGAAGATGAAGGAAGAA 759
QY	1677 AGGACCTGGAAACCATGACCATCTCAGGGCTCAGATGGAAGTTTACTGTTCTGATTTC 1736
Db	760 ATAAAACAAGGAAGTTTACGGCGGCAAGGCTTGAGTGGATGAGTCAAAGGTAGAAGATG 819
QY	1737 ATGCTGAAAGACGACGAGAGAGAAAAATTATGAGGAAGAAAGGAGCAACTGGCATTGACG 1796
Db	820 AAAAAGAAGGGAGTGTAGGATGAGAACGACCAATGAAATGAAAAAGTGGAGAGCAAAAGATGCAAAAG 879
QY	1797 TGGCAGTTCTGCTCAAAAGAGAAATCATGCTTTTCGAAGACGGAGGACGGCAGTCTTGTATGG 1856
Db	880 AAGATGAGAAGAGGAGACAAATGATGATTAAGAAGATGAAAAAGACAGAGCAAGGTTT 939
QY	1857 AGATGCAGAGTCGTATGGGCGGAGAACAAAGTG 1899
Db	940 CTAAAAAGCGTGGGAAAGGACGAGTCTTGAG 972

RESULT 27  
US-10-505-928-344

```
; Sequence 344, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 344
; LENGTH: 4153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-344

Query Match      1.7%; Score 36.2; DB 6; Length 4153;
Best Local Similarity 50.3%; Pred. No. 2.1;
Matches 89; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 1521 TGAACCACTAGTGAAGAACTGCAAGAAAGAGTCAAGAAAGTGGACAGGCGAGTGTGA 1580
DB 1342 TTAATGAAATGAAGTTAAGCAGTGGAAAGAAACAAGCGGAAATAATGAGAAAGAGCACA 1401
QY 1581 AGGAACCTGAGTGAAGAACTGCAAGAAAGGCTCTGGCTTCCAAACAGCTGCAAA 1640
DB 1402 ATGAGTACACAGAACTGGAAGAAAGAAACGAGAAATGTGATGCTAAGACTCAAGAGA 1461
QY 1641 TGAATGAATGAAGCAAAACCATTCGCCAAGCAGGAAGGACCTGGAAACCATGACCA 1697
DB 1462 AGGAAGAGATGATGCAGACCTTAATAATAAATGAAGAGAACTTGAAGAGGAGACTA 1518

RESULT 28
US-10-953-349-20648
; Sequence 20648, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 20648
; LENGTH: 1457
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-20648

Query Match      1.7%; Score 36; DB 6; Length 1457;
Best Local Similarity 48.5%; Pred. No. 1.3;
Matches 99; Conservative 0; Mismatches 105; Indels 0; Gaps 0;

QY 995 GAGGAGTTAACTGTGAGCAGCTCTGCTGTGCTTAAGGAAGGGAATCAGAAAGTGGAG 1054
DB 787 GTGAGACAGCTTGGGAAATGATCAAGTCATAGTAAAGGTGTGATTGACCCAGCAAG 846
QY 1055 AGACTTGAAGTTCACCTCAGGAGGCCAAAGAAAGATTCAGATTTTGAAGAAACA 1114
DB 847 CTAGTTGATTATGTGTACAGAGGACCAAAAGCAAGCTTCTATGTAAGAGGAGGAA 906
QY 1115 AGTAATCGTTCTCAGATTGAAACCCACAGACAGGGGAGCAGAGAAAGAGATGATGAA 1174
DB 907 AAGGAAAGAGCAAGAGAGGAGAGAAAGAGGAGGAGGAGAAAGGAGAGGAGAGAA 966
QY 1175 GAGAAAGCCCGAGACTGTGGA 1198
DB 967 GAGAAAGAGGAGAGATGTTGAA 990
```

## RESULT 29

```
US-10-505-928-758
; Sequence 758, Application US/10505928
; Publication No. US20060088532A1
; GENERAL INFORMATION:
; APPLICANT: Ludwig Institute for Cancer Research et al.
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
; FILE REFERENCE: 28967/39178
; CURRENT APPLICATION NUMBER: US/10/505,928
; CURRENT FILING DATE: 2004-08-27
; PRIOR APPLICATION NUMBER: US 60/363,019
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: PatentIn 3.2
; SEQ ID NO 758
; LENGTH: 1999
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-758
```

```
Query Match      1.7%; Score 36; DB 6; Length 1999;
Best Local Similarity 49.0%; Pred. No. 1.6;
Matches 96; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

QY 1352 TTGAATGAAAGCAAGAGCTTGTATATCTACTACAAAAGTTAGAGCTACAAAGTGGAAAGC 1411
DB 1804 TTGTTTTTAAAGTAAGACTTTTATTAATAACAAATGTTTTGGAGCAAAAAA 1863
QY 1412 ATGCTATCAGAAATCAAAATGGAACAGGCTAAACAGAGGATCAAAAGTCCAATTAAC 1471
DB 1864 AAAAAA 1923
QY 1472 GTGCTACAGATCACACACAAAGCTTCTTCAAGACATAATAATGCAATTCGAAACCAATT 1531
DB 1924 AAAAAA 1983
QY 1532 GAGGAACTAACAGAA 1547
DB 1984 AAAAAA 1999
```

## RESULT 30

```
US-11-217-529-3292
; Sequence 3292, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; CURRENT FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; PRIOR FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3292
; LENGTH: 3279
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-3292
```

```
Query Match      1.7%; Score 36; DB 7; Length 3279;
Best Local Similarity 45.4%; Pred. No. 2.1;
Matches 207; Conservative 0; Mismatches 245; Indels 4; Gaps 2;

QY 1353 TGAATGAAAGCAAGAGCTTGTATATCTACTACAAAAGTTAGAGCTACAAAGTGGAAAGCA 1412
```



Db 995 TGAAGCAAAAGAAAAAGTTAATGATATTTTGAAGTTGAA--TACCATACGAGATGA 1052  
Qy 1413 TCCTATCAGAAATCAAAATGGACAGGCTAAACACAGAGATGAAAGTCCAAATTAACGTG 1472  
Db 1053 TGTATTAAAGAAAGAACTCAAAACGAATATTATAGAGTAGAACCAAGAAATTCGAAGC 1112  
Qy 1473 TGCTACAGATGACACAAACAGCTTCTTCAAGAACATAATATGCAATTTGAAAAACAATG 1532  
Db 1113 AACCATATTGATACAAAGGAGATTGGCGAGAAACCCGAGAAATTCAGAACAACTCA 1172  
Qy 1533 AGGAATAACAGAAAGAGTCAGAAAAAGTGGACAGGCGATGCTGAAGAACTAGTG 1592  
Db 1173 ATTGCTGAAAAAGCGTATTTCAGATATAGATAACAAAAAGAAAGGAATCATCAACA 1232  
Qy 1593 AAAAAGTGAATGCGAGAGAGGCTCTGGCTTCCAAACAGCTGCAAAATGGATGAATGA 1652  
Db 1233 AGAAGAGACCTCCGAGGACTTATTCTGAAATAGACGCAAAAGCAAAATGCCGTAAATCA 1292  
Qy 1653 AGCAA--ACCATTGCACAGCAGAGGAGGACCTGGAAACCATGACCATCTCAGGGCTCA 1710  
Db 1293 TGAATAGAGAGTATACAGAGCAAGCAGACAGATAAACTAAGTCCCTCAATCAACTGA 1352  
Qy 1711 GATGGAAGTTTACTGTTCTGATTTTCATGCTGAAGAGCAGCGAGAGAGAAAAATTCATGA 1770  
Db 1353 TAAATTTGTTATTTTAAATCAAGATCAAGATCTGAAAGAGGTTTCGTGATGCCGTGCTTT 1412  
Qy 1771 GGAAGAGGCAACTGGCATTGCGAGCTGCGAGTTCT 1806  
Db 1413 CATTAGGACCATCCCGAAATGAAGGAGAAAAATCT 1448

RESULT 31  
US-10-488-619-1577  
; Sequence 1577, Application US/10488619  
; Publication No. US20060099578A1  
; GENERAL INFORMATION:  
; APPLICANT: Greenlee, Winner and Sullivan, P.C.  
; TITLE OF INVENTION: Human Mitochondrial DNA Polymorphisms, Haplogroups, Associations  
; FILE OF INVENTION: Physiological Conditions, And Genotyping Arrays  
; CURRENT APPLICATION NUMBER: US/10/488,619  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 3040  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1577  
; LENGTH: 641  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-488-619-1577

Query Match 1.7%; Score 35.8; DB 6; Length 641;  
Best Local Similarity 44.7%; Pred. No. 0.88;  
Matches 139; Conservative 0; Mismatches 172; Indels 0; Gaps 0;

Qy 1251 AAGAGGCTCATCAAAACTCAGGAGCTGAGCTAATGAAGAGAGACTTCAAGAAAAGT 1310  
Db 326 AAAAAACACAAAACACACAGGGAATAAAAAACAAAAAAGAAAAAAGAAAAA 385  
Qy 1311 GTCAGGCCCTTGAAGGAAAAATTTCTGCAATTCATCCATCAGAGTTGAATGAAGCAAGAGC 1370  
Db 386 AAAAAAACAAAAAATAAAAAACCAAAAAAATAAAAAAATAAAAAAAGCAAAAAAAC 445  
Qy 1371 TTGTTTATACAAAAAGTTAGAGTCAAGTGAAGAGCATGCTATCAGAAATCAAAA 1430  
Db 446 CCGCAAGGAAAAAATAACAGGAGAAAAAATAAAAAAATAAAAAAATAAAAAAACCACAAA 505  
Qy 1431 TGAACAGGCTAAAAACAGAGGATGAAAGTCCAAATTAATGTGCTACAGATGACACACA 1490  
Db 506 AAAAAACACAAAAACAAAAAATAAAAAAATAAAAAAATAAAAAAAGAAAAA 565  
Qy 1491 ACAAGCTTCTTCAAGAACATAATAATGCAATTTGAATGAAAAACAATTTAGGAACTTACAGAAAG 1550

Db 566 AAAAAAAAAAAAAAAAAAGAAAAAACAACAAAAAACCAGAGAAAAAACCACAAAA 625  
Qy 1551 AGTCAGAAAA 1561  
Db 626 AAAAAAAAAAAA 636

RESULT 32  
US-10-953-349-4498  
; Sequence 4498, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nickolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 4498  
; LENGTH: 1319  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-4498

Query Match 1.7%; Score 35.6; DB 6; Length 1319;  
Best Local Similarity 47.3%; Pred. No. 1.6;  
Matches 107; Conservative 0; Mismatches 119; Indels 0; Gaps 0;

Qy 472 GAAAGAGCCATGAAGCTAAATAATCAAGCCATGAAGAGGAGATTGAGGAGCTTTCGGC 531  
Db 865 GAAAGGAATATTGATGCACGAGTATCGCCGGAGCAAGCGCGTTGGAGGAGCTTAAAGC 924  
Qy 532 CTGGACACAGAAAAACAGAGGAGAACGCCAGTTTTCAGATACAGACCAAGAACCAA 591  
Db 925 GGAGCTGGAGCGCGGTTCTCGCGTGGCGGTGTTGGTGGGAGAGAGGGAGGAGGAGA 984  
Qy 592 AGAGCGCTCTAATGGCTTTGAGTCATGAGATGAGAAATGAAAGGAGAGCTTGGAAAACT 651  
Db 985 GGAGACACAGAGGAGGAGCTGAGAGAGAGTTGAGATCTGAAGGGTATTTTGGTAATTT 1044  
Qy 652 AAAAGGAAATCAGAAAGTCAATCTGAGACCCCACTGATGACTCC 697  
Db 1045 AAGGAATGGACAGAGAGTATAGTGGCGCAAAATCGATGATTTCTTC 1090

RESULT 33  
US-11-136-524-59  
; Sequence 59, Application US/11136524  
; Publication No. US20060094034A1  
; GENERAL INFORMATION:  
; APPLICANT: BROUSSEAU, Roland  
; APPLICANT: HAREL, Josee  
; APPLICANT: BEKAL, Sadjia  
; TITLE OF INVENTION: ARRAY AND USES THEREOF  
; FILE REFERENCE: 86369-3  
; CURRENT APPLICATION NUMBER: US/11/136,524  
; CURRENT FILING DATE: 2005-05-25  
; NUMBER OF SEQ ID NOS: 182  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 59  
; LENGTH: 2126  
; TYPE: DNA  
; ORGANISM: Escherichia coli  
US-11-136-524-59

Query Match 1.7%; Score 35.6; DB 7; Length 2126;  
Best Local Similarity 52.7%; Pred. No. 2.1;  
Matches 77; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

Qy 1758 AGAAAAATTCATGAGGAAAGGAGCACTGGCAATTCAGCTGGCAGTTCTCTGTAAGAGA 1817



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RESULT 38
US-10-953-349-19713
; Sequence 19713, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nikolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLY
; TITLE OF INVENTION: ENCODED THERAPY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19713
; LENGTH: 1476
; TYPE: DNA
; ORGANISM: Glycine max
US-10-953-349-19713

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Qy	1044	AGRAGGTGGAGACACTTGAAGTTTGCACCTCAAGAGGAGCCCAAGAAGAAGAGTTTCAGATTTTG	110
Db	132	AGAGGAAGAAGAGCGGATGATGATGATGACGTGGAAAGCAGAAGCAGACAGCTTCAGGTTGGA	191
Qy	1104	AAAAAGAAAAACAAGTAAATCGTTTCTTGAGATTGAAACCCACAGACAGAGGGG	1150
Db	192	AGAAGAAAAACGAGAACCGACGTCGGAGAGAGAGAGGAAGGAGAAGAAAGGAG	238

RESULT 39

US-10-505-928-326

; Sequence 326, Application US/10505928

; Publication No. US20060088532A1

; GENERAL INFORMATION:

; APPLICANT: Ludwig Institute for Cancer Research et al.

; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; PRIOR FILING DATE: 2002-03-07

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

```
; SEQ ID NO 326
; LENGTH: 10211
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-505-928-326

Query Match      1.7%; Score 35; DB 6; Length 10211;
Best Local Similarity 40.9%; Pred. No. 8.1;
Matches 266; Conservative 0; Mismatches 385; Indels 0; Gaps 0;

QY 968 GATGGGCGAAGTAATCTTCGACATCAGGAGTAATCTGAGCCAGCTCTGCTGTC 1027
DB 7537 GATGAGGCGAAATAATATATATGTTTGTGCAATCTTCAGTGAATGGCCTCAITCAAGAA 7596

QY 1028 CTAAGGGAAGGAATCAAGAGGTGGAGAGACTTGAAGTTGCACCTCAAGGAGGCCAAAGAA 1087
DB 7597 GTAGAGATGCGACAGCAAACTGGAGAGAGAGATGAAGAAATCAGTAGACTGAAAAAT 7656

QY 1088 AGAGTTTCAGATTTTGAAGAAACAAAGTAATCGTTCTGAGATTGAAACCCAGACAGAG 1147
DB 7657 CAAATTCAGAGACCAAGAGCAGCTTGTCTCTAAACTGTCCAGGTGGAAGGAGACGACCA 7716

QY 1148 GGGAGCACAGAGAGAGAGATGATGAGAGAGAAAGCCCGGAGACTGTTGGNAGCGAAGTG 1207
DB 7717 CTTTGGAGGAGCAAACTTAGAACTGAGAAATCTGACAGTGGAAATGGAGCAGAGATC 7776

QY 1208 GAAGCAGCTGAACCTCCAGGTGACATCTCTGTTTAAGGAGCTTCAAGAGGCTCATACAAA 1267
DB 7777 CAAGTGTACAAATCAAAATATGCTCTTTGAGGACACATAGAAATGCTGCAGAGTTCT 7836

QY 1268 CTCAGCGAAGCTGAGCTAATGAAGAGAGAGACTTCAAGAAAGTGTCAAGGCCCTTTGAAAG 1327
DB 7837 TACAAGATCTAGAGATGAGCTTGAATTGACAAATATGGACAAATGTCTCTTTGTTGAA 7896

QY 1328 AAAAATCTGCANTTCATCAGAGTTGAATGAAGAAAGCAAGAGCTTTGTTTATACAA 1387
DB 7897 AAAGTAACAAATGACTGCAAGGAAATCTGAGCTGCAGAGGGAATGCATGAGATGCCA 7956

QY 1388 AAGTTAGAGCTACAAAGTGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTTAAACA 1447
DB 7957 CAGAAACAGCAGAGCTGCAAGAGAACTCAGTGGAGAGAAAATAGCTAGCTGGAGAG 8016

QY 1448 GAGGATGAAAAGTCCAAATTAACCTGTGCTACAGATGACACACAAAGCTTTCTTCAAGAA 1507
DB 8017 TTGCAGTACTGTTGGAGAGAAATGAAGAGCAGCAAGATCAATTTGAAGGAGCTCACACTA 8076

QY 1508 CATATATGCAATTTGAAAACAAATTTGAGAGAACTAACAAGAAAGAGTCAAGAAAAGTGAC 1567
DB 8077 GAAAATAGTGAATTTGAAGAGAGCCTAGATTGCTATGCACAAAGACCAGGTGGAAGAAAG 8136

QY 1568 AGGCAGTCTGAAGGAACTGAGTGAAAACCTGGAACCTGGCAGAGAGGCT 1618
DB 8137 GGGAAAGTGAGAGAGAAATAGCTGAATATACGTACCGCTTTCATGAAGCT 8187

RESULT 40
US-11-236-238-1
; Sequence 1, Application US/11236238
; Publication No. US200601053641
; GENERAL INFORMATION:
; APPLICANT: Petrukhin, Konstantin
; APPLICANT: Caskey, C. Thomas
; APPLICANT: Metzker, Michael
; APPLICANT: Claes, Wadellus
; TITLE OF INVENTION: BEST'S MACULAR DYSTROPHY GENE
; FILE REFERENCE: 201779P
; CURRENT APPLICATION NUMBER: US/11/236,238
; PRIOR FILING DATE: 2005-09-27
; PRIOR APPLICATION NUMBER: US/09/622,964
; PRIOR FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: PCT/US99/03790
; PRIOR FILING DATE: 1999-02-22
; PRIOR APPLICATION NUMBER: 60/112,926

; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: 60/075,941
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 16125
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(16125)
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 2166, 2167, 2168, 2169, 2170, 2171, 2172, 2173, 2174, 2175,
; LOCATION: 10444, 10445, 10446, 10447, 10448, 10449, 10450, 10451
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 10452, 10453, 15338
; OTHER INFORMATION: n = A,T,C or G
US-11-236-238-1

Query Match      1.7%; Score 34.8; DB 7; Length 16125;
Best Local Similarity 58.8%; Pred. No. 12;
Matches 60; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 733 CCAGCTCAGACCCAGGTGTGAGGCTACAGCAGAGAGGAGGAGCTTTGGGCATCGT 792
DB 3549 CCAGCTCAGGCGCCAGTGCACCACTCACTACAACTAAGCTGGGCTCCTGACCAGCTC 3608

QY 793 GTCTGAATGCAGCTCAAGCTGAAGTCCAGCGGCTCTCTCAGA 834
DB 3609 CTGGGCACCTGGAGCTGAGGCTGCCGCTGGGGCTGGGCAGA 3650

RESULT 41
US-11-217-529-78785
; Sequence 78785, Application US/11217529
; Publication No. US20060099612A1
; GENERAL INFORMATION:
; APPLICANT: SUNTORY LIMITED
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: S-38-285
; CURRENT APPLICATION NUMBER: US/11/217,529
; PRIOR FILING DATE: 2005-09-02
; PRIOR APPLICATION NUMBER: US 10/932,182
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 78785
; LENGTH: 1992
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-11-217-529-78785

Query Match      1.7%; Score 34.6; DB 7; Length 1992;
Best Local Similarity 58.1%; Pred. No. 3.9;
Matches 61; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

QY 1420 AGAAATCAAAATGGAACAGGCTAAACACAGAGGATGAAAGTCCAAATTAAGTGTGTACA 1479
DB 180 AAAAGATAACTGAATGAGATGAAGTCCAAATGTAAATTTACGATTAAATGTGGTACT 239

QY 1480 GATGACACACAAAGCTTTCTTCAAGAACATAATAATGCAATTGAA 1524
DB 240 GACTACTCTACAGAAGCTTGGTACATCCGATAATCTCTGCTTTGTA 284
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Db 991 CCCACACCTGAGGAGACTCAGAAACACACAGCCTGATGAGGAGTAAG 1036

RESULT 49

US-11-217-529-5434

; Sequence 5434, Application US/11217529

; Publication No. US20060099612A1

; GENERAL INFORMATION:

; APPLICANT: SUNTORY LIMITED

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: S-38-285

; CURRENT APPLICATION NUMBER: US/11/217,529

; CURRENT FILING DATE: 2005-09-02

; PRIOR APPLICATION NUMBER: US 10/932,182

; PRIOR FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 5434

; LENGTH: 2349

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-11-217-529-5434

Search completed: May 30, 2006, 00:04:02

Job time : 42 secs

Query Match 1.6%; Score 34; DB 7; Length 2349;

Best Local Similarity 46.9%; Pred. No. 6.3;

Matches 106; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 1345 ATCAGAGTTGTAATGAAAGCAAGAGCTTCTTATACACAAAGTTAGAGTACAGT 1404

Db 1068 ATCAGAGCAACAAAGAAATCGATGCTGCTGCTGAAACAAATAGAAAGATCAAGC 1127

QY 1405 GGAAGCATGCTATCAGAAATCAAAATGGAACAGGCTAAACACAGAGGATGAAAGTCCAA 1464

Db 1128 TTACTGAACGTTCAAGATCAATGAAAGCAAGGTCATCTAATAATTGAAACGCCTC 1187

QY 1465 ATTAAGTGTGCTACAGATGACACACAAAGCTTCTTCAAGAACATAATAATGCAATTGAA 1524

Db 1188 CTTAATAGAGGAGTGAAGCTGCTGCTCCAAAGTTTAAATTGATCAACAAATGGATTGGAG 1247

QY 1525 AACAAATTGAGGAACTAACAGAAAGAGTCAGAAAGTGGACAGG 1570

Db 1248 CACTATTGAAACTAATAAAGTGACAGAAAGGGAATATG 1293

RESULT 50

US-10-953-349-39192

; Sequence 39192, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: ENCODED THERBY

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 39192

; LENGTH: 987

; TYPE: DNA

; ORGANISM: Zea mays subsp. mays

US-10-953-349-39192

Query Match 1.6%; Score 33.8; DB 6; Length 987;

Best Local Similarity 49.2%; Pred. No. 4.2;

Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 459 AGAACCAACAGCTGAAGAGCAAGCCATGAAGCTAATAATCAAGCCATGAAGGAGATTG 518

Db 393 AGAAACGCAAGAAAGATAGGAAACAAAGACAAAGATAAAGGCGCAAGAAA 452

QY 519 AGGAGCTTTTCGGCTGGACAGAGAAACAGAGGAGAAAGCCAGTTTTTTTGAGATACAGA 578

Db 453 AGGATGTATCGGAACCAAGGGTGCAAGAGGATGAAGATGGTAAGAAAGAAAGAGCGCGATG 512

QY 579 GCAGAAAGAAAGAAAGAGCGCTCTAATGGCCTTGGAGTCATGAGAAATGAGAAATTTGAAGGAAG 638

Db 513 GCGATGAAGACGAGAGAGGTAAGAGGAGGACACAGAAAGAAAGAGAGAGAGGAAAC 572

QY 639 A 639

Db 573 A 573